

1	74.4	12.5	372	7	US-10-282-122A-25335	Sequence 2335, A
2	50	8.4	2466	6	US-10-156-761-5788	Sequence 5788, Ap
3	50	8.4	9025608	6	US-10-156-761-1	Sequence 1, Appli
4	47.6	8.0	2256646	7	US-10-470-565-1	Sequence 1, Appli
5	47.4	7.9	548	7	US-10-437-963-94550	Sequence 94550, A
6	46.6	7.8	1389	8	US-10-411-910A-255	Sequence 255, App
7	46.6	7.8	1389	8	US-10-411-910A-257	Sequence 257, App
8	46.2	7.7	1209	6	US-10-369-493-32038	Sequence 32038, A
9	46.2	7.7	1509	8	US-10-411-910A-264	Sequence 264, App
10	45.8	7.7	2209	7	US-10-437-963-69229	Sequence 69229, A
11	45.2	7.6	2238	7	US-10-437-963-97363	Sequence 97363, A
12	45.2	7.6	3743	9	US-10-502-351-1	Sequence 1, Appli
13	44.4	7.4	1445	7	US-10-437-963-35783	Sequence 35783, A
14	44.2	7.4	1000	7	US-10-389-566-49	Sequence 49, Appl
15	44.2	7.4	1377	6	US-10-369-493-39791	Sequence 39791, A
16	44.2	7.4	1395	6	US-10-369-493-39403	Sequence 39403, A
17	44.2	7.4	1404	6	US-10-369-493-39036	Sequence 39036, A
18	44.2	7.4	2055	7	US-10-389-566-235	Sequence 235, App
19	44	7.4	1368	7	US-10-437-963-7459	Sequence 7459, Ap
20	44	7.4	9338	10	US-11-097-743-32926	Sequence 32926, A
21	43.8	7.3	1507	8	US-10-425-115-108376	Sequence 108376, A
22	43.8	7.3	2978	8	US-10-739-930-4715	Sequence 4715, Ap
23	43	7.2	681	7	US-10-767-701-23705	Sequence 23705, A

QY 415 GACTTNCCCAACAAGTGGCCACC 437
Db 7015647 GCCCGGCACGAGAGGGCCGTACC 7015669

RESULT 4
US-10-470-565-1/c
; Sequence 1, Application US/10470565
; Publication No. US20040126870A1
; GENERAL INFORMATION:
; APPLICANT: Societe des Produits Nestle S.A.
; TITLE OF INVENTION: NCC2705 - the genome of a Bifidobacterium
; FILE REFERENCE: 80290/NO
; CURRENT APPLICATION NUMBER: US/10/470,565
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: EP 01102050.0
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2256646
; TYPE: DNA
; ORGANISM: Bifidobacterium longum
US-10-470-565-1

Query Match 8.0%; Score 47.6; DB 7; Length 2256646;
Best Local Similarity 44.6%; Pred. No. 0.003;
Matches 185; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

QY 15 CCGCGCCACCAGCAGCAGACGCGGAGCGGGATGCGGGCGGAGAGCTGTTGA 74
Db 1432814 CGTCTCTACTTTCACCGCAGGATGGGTATGAGTGGCCACAGGCAACCCCAAGAACGT 1432755

QY 75 TGACCTGGCGGCGCAGAGGATGAGCTGGGTGACCTTCTAGATAAGTGTCT 134
Db 1432754 CGATGAGAACGACCTGTGCGGTCTGAACGTTCCCGTCGAGACCGGACCGCTCGAGGAAGA 1432695

QY 135 GGCTGACCCGGAGCTGTGTCCTTCTTCAGTCCCTGGACATGCAAGAGCAGAGATGAA 194
Db 1432694 GGCCATCAACAGACCGCCAGCAGTGCAGGCGGAGGAGGAGCATCACCATCCA 1432635

QY 195 GAGGTCAAGTTCATGAGCTTCTGTTGGCGGAGCAGCAATACAGGGCCGAGCAT 254
Db 1432634 GTCTCTCAAGCAGCAGACCGACGCCACCCACTGTGTGACCGGCAAGGCGGAGCTTT 1432575

QY 255 GTACGACGACACGCCCATCTGTCTAAGGGCCAGCGCTGGACCCGACCTTTGACAA 314
Db 1432574 CTTCCCGGATTCCTCCGTTGTGCGGTACGCCATCGCCAGACCGATGGTCACTGGAACA 1432515

QY 315 GATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAGCAGAGTGTATCCA 374
Db 1432514 GCTCGGCAAGGACTTCGATGAGTGGGAGCCGATCGCCATCAAGAGGGGCAATCCA 1432455

QY 375 GCACGCGCGCGAGTGGTGGATGCCACCGCGGAGCAATTTGATNCCCAACAC 429
Db 1432454 GACCACCGAAGCGCTGCGAAGGCGCATCAAAAGCTCATGGACGCGGACCTAC 1432400

RESULT 5
US-10-437-963-94550
; Sequence 94550, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 94550
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_9282C.1
US-10-437-963-94550

Query Match 7.9%; Score 47.4; DB 7; Length 548;
Best Local Similarity 50.4%; Pred. No. 0.0027;
Matches 114; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 216 CGTGTTCGCGGAGCAGACCAATACAAAGCGCGGAGCATGTACGACGACGACGCGCCATCT 275
Db 194 CGTGTTCGCGGCGCCGACGCGCGCGTCCGGCGGGCATGTTCCGCGACCTCGCCCGGTG 253

QY 276 GGTCAAGGGCCACGCGCTGGGACCAACCGCCACTTTTGACAAGATCAAGCAGTACTTTGGAGA 335
Db 254 GTCATGCTCCACATGCTCAACTTCACGAGGCGGTGACCATGACGAAGCGCGCGCGA 313

QY 336 GACGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCAGACGCGCGCGGAGTGGTGA 395
Db 314 GAAAGCTCTTCAAGGTGCTCGACATGTACGAGGCCACCGCGCGCGTCCCGGTCTATCGA 373

QY 396 GTCCACCGCGCAGCAATTTGACTTNCCTCAACAACTGCGCACCCAC 441
Db 374 GCGCTTCTCCACCGCGCAGCAGCGCAACAACAGCAGCAGCCGCTGACC 419

RESULT 6
US-10-411-910A-255
; Sequence 255, Application US/10411910A
; Publication No. US2004020256A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
; FILE REFERENCE: H2041203-P
; CURRENT APPLICATION NUMBER: US/10/411,910A
; CURRENT FILING DATE: 2003-04-12
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 255
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-411-910A-255

Query Match 7.8%; Score 46.6; DB 8; Length 1389;
Best Local Similarity 44.9%; Pred. No. 0.0065;
Matches 175; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

QY 40 GCGAAGCGGATCGGCGCGCAAGAGCTGTTGATGACCTGGGCGGCGGAGAGGCGATG 99
Db 685 GTGGTGGTGGCCCTGTCTACGACGAAGAGCTGGAGGCGCTGCGGAGGGCTGAGCACC 744

QY 100 AAGCTGGCGTTGACACTTTTACGATAAGTGTGTGCTGACCCGAGAGTGTGTCCTTC 159
Db 745 ACCCTGAACGCGCGCGCGGACCCGACTGCTGTGACGAGCGGCGGAGATGCCCGAGATC 804

QY 160 TTCAGTCCCTGGGACATCAAGAGCAGAGATGAGAGCTCAAGTTCATGAGCTTCGTG 219
Db 805 ATGGAGCAGAGCGACCTGAGCGTGAAGGACATCGCCGTGGAGACACCTGTTCGGCAGATG 864

QY 220 TTGCGGAGCAGACCAATACAAAGGCGGAGAGCTGTACGAGCAGCAGCCCATCTGGTTC 279
Db 865 AAGGAGTGGCGTGCAGCGGCAACGACGCGGTGAGCAGGAGCGGCACTGGCCCACTG 924

QY 280 AAGGCGCACGCGCTGGACCAACCGCCACTTTTGACAAGATCAAGCAGTACTTTGGAGAGC 339

Db 925 TTCCGCCACGCCCAAGGAGCTGTTCCGGCAGCAGCTGGAGGAGATCACTACCGCGC 984
QY 340 CTGCAAGAGTGGCGCTCAAGCAGGATGTATCAGCAGCCCGCGGAGTGGTGGATCC 399
Db 985 TTCCGCAACAAAGACTTCCACGAGGTGACCCCTGGAGAAGAACGGCGAGGTGCTGCGC 1044
QY 400 ACCCGCGAGGAATTTGACTTNCACCAAC 429
Db 1045 TTCCGCCCGCCTACGGCTTCCGCAATC 1074

RESULT 7

US-10-411-910A-257
; Sequence 257, Application US/10411910A
; Publication No. US20040209256A1
; GENERAL INFORMATION:
; APPLICANT: Dillion, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
; CURRENT APPLICATION NUMBER: US/10/411,910A
; CURRENT FILING DATE: 2003-04-12
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 257
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-411-910A-257

Query Match 7.8%; Score 46.6; DB 8; Length 1389;
Best Local Similarity 44.9%; Pred. No. 0.00065;
Matches 175; Conservative 0; Mismatches 215; Indels 0; Gaps 0;
QY 40 GCGGAAGCGGGATCGCGGCCAAGAAGCTGTTTATGACCTGGCGCGCAGAAAGCAG 99
Db 685 GTGCTGTGGCCCCCTGCTACGACAAGAAGCTGGAGGCCCTGGCGAGGGCCTGAGCAC 744
QY 100 AAGTGGCGGTGACACCTTCTAGGATAAGTGTGCTGCTGACCGGAGTGTGCTGCCCTTC 159
Db 745 ACCCTGAACCGCGCCCGCGCCGACCTGCTGCTGACCGCGCGGAGATCGCCCAATC 804
QY 160 TTGAGTCCCTGGACATGCAAGAGCAGAAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTG 219
Db 805 ATGAGCAGAGCGACCTGAGCGTGAAGACATCGCCGTGACACCTGTTCCGGGCATG 864
QY 220 TTTGGCGGAGCAGACCAATATCAAGGGCCGAAGCATGTACAGCAGCATCGCCCATCTGGTC 279
Db 865 AAGGAGTGGCGGTGACGCCCGACGCGCGTGAAGCAGCGACGCGCCACCTGGCCACGTG 924
QY 280 AAGGCCACCGCCTGGACCCACCGCCACTTTGACAGATCAAGCAGTACCTTGGAGAGACG 339
Db 925 TTCCGCCACCGCGCCCAAGGAGCTGTTCCGGCGAGCAGCGTGGAGGAGATCACCTACCGCGCC 984
QY 340 CTGCAAGAGTGGCGCTCAGCAGGATGTATCCAGCAGCCCGCGGAGTGGTGGATCC 399
Db 985 CTGCGCAACAAAGACTTCCACGAGGTGACCCCTGGAGAAGAACGGCGAGGTGCTGCGC 1044
QY 400 ACCCGCGAGGAATTTGACTTNCACCAAC 429
Db 1045 TTCCGCCCGCCTACGGCTTCCGCAATC 1074

RESULT 8

US-10-369-493-32038
; Sequence 32038, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 32038
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Thermobifida fusca
; US-10-369-493-32038

Query Match 7.7%; Score 46.2; DB 6; Length 1209;
Best Local Similarity 55.2%; Pred. No. 0.00083;
Matches 90; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 248 GAAGCATGTACGACGACACGCCCATCTGCTCAAGGGCCACGCGCTGGACCACCGCCACT 307
Db 86 GCACCCCTGCTCTTCGACGAAGTGTGTTGGTGGAGCGCGCCGCGAGGAGCAGACCTGT 145
QY 308 TTGACAAAGATCAAGCAGTACCTTGGAGACAGCTGCAAGAGATGGCGGTCAAGCAGATG 367
Db 146 TCGTCCAGCTCCTGGCGGACCGGGGGTGACCGTGCATGAATTCGCGAGCCTGCTCGCG 205
QY 368 TGATCCAGCAGCGCGCGGAGTGGTGGAGTGCACCCGCGACGA 410
Db 206 AGACTCTGCATATCCCGAGGCGAAGAGTTTATCTCTCAGCA 248

RESULT 9

US-10-411-910A-264
; Sequence 264, Application US/10411910A
; Publication No. US20040209256A1
; GENERAL INFORMATION:
; APPLICANT: Dillion, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
; FILE REFERENCE: H2041203-P
; CURRENT APPLICATION NUMBER: US/10/411,910A
; CURRENT FILING DATE: 2003-04-12
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 264
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-411-910A-264

Query Match 7.7%; Score 46.2; DB 8; Length 1509;
Best Local Similarity 46.2%; Pred. No. 0.00089;
Matches 153; Conservative 0; Mismatches 178; Indels 0; Gaps 0;
QY 54 CGGCGCAGAAAGCTGTTTATGACCTGGCGCGCAGAGCATGAAGTGGCGGTGA 113
Db 846 CGGCGCGCAGCGCTTGACGCGCAAGATCGCCCCCTGACAGCAGACCTGGCGCGCG 905
QY 114 CACCTCTTAGATAAGTGTGCTGACCGGAGTGTGCTGCTTCTTCAGTCCCTGGA 173
Db 906 CGGCGAGATCGCCAGATCATGAGCAGGCGGCGACCTGAGCGTGGCGACCGCCGCTGGA 965
QY 174 CATGCAAGAGCAGAAAGATGAAGCAGGTCAAGTTTCATGAGCTTCTGTTTGGCGGAGCAGA 233
Db 966 CACCTGTTCCGGCAGCCTGAAGAGGACAAAGTTGACCCGCCACGACGCGGCCAGCAGCA 1025
QY 234 CCAATACAGGGCGGAGCATGTACGACGACACGCCCATCTGCTCAAGGGCCACCGCCT 293
Db 1026 CGGCCACCTGGCCACATCTTCGCCACGCGCGCAAGAGCTGTTCACAGGAGCTGGA 1085
QY 294 GGACACCGCCACTTTGACAAAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGG 353
Db 1086 GGAGGTGACCTACCGCGCCCTGCGCAACAAGGACTTCCAGGAGGTGACCTGGAGAGAA 1145

QY 354 CGTCAAGCAGGATGTGATCCAGCACGCCGCC 384
Db 1146 CGCGAGGAGTGTGCTCGCTTCGCCGCCGCC 1176

RESULT 10

US-10-437-963-69229
; Sequence 69229, Application US/10437963
; Publication No. US20040123343A1

GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 69229

; LENGTH: 2209

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_69918C.1

US-10-437-963-69229

Query Match 7.7%; Score 45.8; DB 7; Length 2209;
Best Local Similarity 46.1%; Pred. No. 0.0013;
Matches 152; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 110 TTGACACCTTTACGATAGTGTCTGGTGTGACCGGAGCTGTGCGCTTCTTCGAGTCCC 169
Db 400 TCGACTACGTGTGTCTCAAGAGCGACGACCGGAAGCTCCCGACCGACCTGTGCGGG 459
QY 170 TGGACATCAAGAGCAGAGATCAAGCAGTCAAGTTCATGAGCTTCGTTGGCGGAG 229
Db 460 AGATCATCAGCGGACAGAGCTCTGGGGTGGAGGAGTACAGTTCCTCTCAAGGTCA 519
QY 230 CAGACCAATACAGGGCGGAGCATGTACGACACACGCCCATCTGGTCAAGGGCCACG 289
Db 520 TCGTCACTCCGATCGGCGAGGACCTACGGGCGCGGACATCGGCGGGCGG 579
QY 290 GCGTGGACCAACCGCCACTTTGACAGATCAAGCAGTACCTTTGAGAGAGCGTTGCAAGAGA 349
Db 580 ACGCCCGCCCGACCGCTCGCGGAGGGATGGAGGAGATGGACGAGAGCTTCCACGCCG 639
QY 350 TGGGGCTCAAGAGGATGTATCCACACCGCGCGGAGTGTGGAGTCCACCGCGGAG 409
Db 640 TCGTCAAGAGTGTTCGCGCGCTCGTCCGCGCGCGCGCGCGCGCGCGCGCG 699
QY 410 AATTGACTTNCACCAACTCGGCGACCCA 439
Db 700 ACCTCGACCTCTCTGCTCAAGCTGTCCA 729

RESULT 11

US-10-437-963-97363/c

; Sequence 97363, Application US/10437963

; Publication No. US20040123343A1

GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 97363
; LENGTH: 2238
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95374C.1

US-10-437-963-97363

Query Match 7.6%; Score 45.2; DB 7; Length 2238;
Best Local Similarity 50.2%; Pred. No. 0.0021;
Matches 110; Conservative 0; Mismatches 109; Indels 0; Gaps 0;
QY 216 CCGTTTGGCGGAGCAGACCAATACAGGGCGGAGCATGTACGAGCAGCACGCCCATCT 275
Db 1249 CCGTTTGGCGGCTGCGAGCGCGCTCGCGCGCGCATCTTCGTCGACCTCGCGCGCTG 1190
QY 276 GGTCAAGGGCCAGCGCTGGACACCGCATCTTTCACAGATCAAGCAGTACCTTGAGA 335
Db 1189 CGCCATGTCTCAGATGCTCAACTTCAACGAGCGCTGCGCATGACGAGCGCGCGCG 1130
QY 336 GACGCTGCAAGAGATGGCGCTCAAGCAGGATGTATCCAGCAGCGCGCGCGAGTGGTGA 395
Db 1129 GAAGCTCTTCAAGTGTCTGACATGTACGAGCGCGCTCGCGAGCGCGCGCGCATCGA 1070
QY 396 GTCCACCGCGGACGAAATTTGACTTNCCTCCCAACAACTGCGC 434
Db 1069 CGCTTTCATCGCGCTGTCTCCACCGACCGCGCGCGC 1031

RESULT 12

US-10-502-351-1

; Sequence 1, Application US/10502351

; Publication No. US20050155088A1

GENERAL INFORMATION:

; APPLICANT: Zhang, Lian Hui

; APPLICANT: Xu, Jin Liang

; TITLE OF INVENTION: Ralstonia AHL-Acylase Gene

; FILE REFERENCE: 2977-154

; CURRENT APPLICATION NUMBER: US/10/502,351

; CURRENT FILING DATE: 2004-07-23

; PRIOR APPLICATION NUMBER: PCT/SG02/000011

; PRIOR FILING DATE: 2002-01-23

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1

; LENGTH: 3743

; TYPE: DNA

; ORGANISM: Ralstonia sp.

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (16)..(16)

; OTHER INFORMATION: n is a, c, g, or t

US-10-502-351-1

Query Match 7.6%; Score 45.2; DB 9; Length 3743;
Best Local Similarity 45.2%; Pred. No. 0.0024;
Matches 164; Conservative 0; Mismatches 199; Indels 0; Gaps 0;
QY 69 GTTGTGATGACCTTGGCGGCGGAGAGGATGAAGTGGCGGTGACACCTTTACGATAA 128
Db 2055 GCTCGAGGTGATGGCGGCTCGATCGCGCTTCCGGTGGTGGAGCATCGGCTTCAACA 2114
QY 129 GGTGTGCTGACCGGAGCTGCTGCCCTTCTTCAGTCCCTGGACATCAAGAGAGAA 188
Db 2115 GGACGTGGTGGAGCGACACCGTCTCCACCGCGCGCGCTTTCACCTTGTTCGAAC 2174

Qy	189	GATCAACAGGTCAAGTTTCATGACCTTCGTGTTTGGCGGAGCAGACAACATACAAAGGGCCG	248
Db	2175	GCTGGCGAAGGCAACCCGACACCTACTCTGTTGACGCGCACCGCCGACAAAGATGACAC	2234
Qy	249	AAGCATGTACGACGACACACGCCCATCTCGTCAAGGGCCACGGCTGGACCAACCGCCACTT	308
Db	2235	CCGACACGTCGCTTCGACGCTCAAGCTGCGGACGGCGCTCTCGAGCGCCGACGCACAC	2294
Qy	309	TGACAAGATCAAGCAGTACCTTGGAGAGACGCTCAAGAGATGGCGTCAAGCAGGATGT	368
Db	2295	CTTCTACGACACCATCTACGGCCGCTGCTCGATCCGAGCGCGGCATCCGCTGCAC	2354
Qy	369	GATCCAGCAGCCCGCGAGTGTGTGAGTCCACCCGCGACGAATTTGACTNCCCAACAA	428
Db	2355	CACGCAAAAGGCTTACGCCCTTGCGCCGCGCCACCCGCAACAACACGCGCTCGGTGCGAG	2414
Qy	429	CTG	431
Db	2415	CTG	2417

```

RESULT 13
US-10-437-963-35783
; Sequence 35783, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 35783
; LENGTH: 1445
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_39672C.1
US-10-437-963-35783

```

Query Match	7.4%	Score 44.4	DB 7	Length 1445
Best Local Similarity	46.5%	Pred. No. 0.0033		
Matches 141	Conservative 0	Mismatches 162	Indels 0	Gaps 0
Qy	139	GACCCGAGCTGCTGCCCTTCTTGAGTCCCTGGACATGCAAGAGCAGAAGATGAAGCAG	198	
Db	167	GACCGTCGCACTGGCCGACGACCTCGACCCGGAGCTCGCGAGCTCGAGCCCAAGCTG	226	
Qy	199	GTCAGTTCATAGCTTCGTGTTTGGCGGACAGACACCATACAGGGCCGAAGCATGTAC	258	
Db	227	GCCAGCTGGCCGCGCGGGCAAACCCGGGCGTCTGCAGGTGCGACGCCGTATCAGAGAC	286	
Qy	259	GACGACACACGCCCATCTGGTCAAGGGCCACCGGCTGGAACACCGCCACTTTTGACAAATC	318	
Db	287	GACGCTGGACGCACATGGTCAATGACACTCTGCTCCGSCCCGACCTGCTCGACTGGATC	346	
Qy	319	AAGCAGTACTTTGGAGACACGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGAC	378	
Db	347	CGCTCCGCGCGCGCGCCCGTCCCGAGCCCGTCCGCGCGCGCGTGTGTCGCGAGCTC	406	
Qy	379	GCCGCGGAGTGTGGAGTCCACCCGACAGAAATTTGACTTNCACAAACACTGGCGCACC	438	
Db	407	GCAGAGGCGCTCGCGCACTGCATGCACACGCGCGGGGTGCGCCACCGGACGTCGAAGCCCGAC	466	

```

Qy 439 AAC 441
Db 467 AAC 469

RESULT 14
US-10-389-566-49/c
; Sequence 49, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Zea mays
US-10-389-566-49

Query Match 7.4%; Score 44.2; DB 7; Length 1000;
Best Local Similarity 53.8%; Pred. No. 0.0034;
Matches 91; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 66 GCTGTTTGATGACCTGGGGCGGCGAGCATGAGCTGCGGTTTGACACCTTCTACGA 125
Db 676 GCAGTTTCATCGCGCGGTCCACGCGCGCGAGATGCTCACGGTAGAGGGCTACCACGA 617

Qy 126 TAAGTGCTCGCTGACCCCGAGCTGCTGCCCTTCTTCGAGTCCCTCGACATGCAAGACGA 185
Db 616 CATCGTGTGCGGACGCGAAGCGCTGTGCGCGCGAGATCTCTGGGTGACCGCCCC 557

Qy 186 GAAGATGAAGCAGGTCAAGTTCATATGAGCTTCGTGTTTGGCGGAGCAAC 234
Db 556 GACGCTCAAGAAGTCGCGAGAGGTGGGCGCGTGTGTGTCGTCGCCGAC 508

```

RESULT 15
 US-10-369-493-39791
 ; Sequence 39791, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 39791
 ; LENGTH: 1377
 ; TYPE: DNA
 ; ORGANISM: Xanthomonas campestris
 US-10-369-493-39791
 Query Match 7.4%; Score 44.2; DB 6; Length 1377;
 Best Local Similarity 48.2%; Pred. No. 0.0037;

Matches: 124; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY	151	CTGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAAGATGAAGCAGGTCAAGTTTCATG	210
Db	784		
QY	211	AGCTTCGTGTTTGGCGGAGCAGACCAATACAAAGGGCGGAAGCATGTACGACGACACGCC	270
Db	844		
QY	271	CATCTGCTCAAGGGCCACGGCCTGGACCAACCGCCACTTTGACAAAGATCAAGCAGTACCTT	330
Db	904		
QY	331	GGAGAGCAGTGCAGAGATGGCGCGTCAAGCAGGATGTGATCCAGCACCGCCCGGAGTG	390
Db	964		
QY	391	GTGGAGTCCACCGCGA	407
Db	1024		
		GTGGTGGCGCTGGCGGA	1040

Search completed: February 27, 2006, 22:34:13
Job time : 754 secs

This Page Blank (uspto)

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	41.6	7.0	1280	12	US-11-219-995-4	Sequence 4, Appli
2	40.8	6.8	1134	8	US-10-517-939-295	Sequence 295, App
3	37.8	6.3	1027	12	US-11-136-527-94	Sequence 94, Appl
4	37	6.2	859	7	US-10-714-887-161	Sequence 161, App
5	37	6.2	1222	12	US-11-136-527-3173	Sequence 3173, Ap
6	36.8	6.2	7474	12	US-11-069-834-49	Sequence 49, Appl
7	36.6	6.1	2644	12	US-11-136-527-2717	Sequence 2717, Ap
8	36.4	6.1	581	6	US-09-923-055A-662231	Sequence 662231,
9	36.4	6.1	619	12	US-11-136-527-3549	Sequence 3549, Ap
10	36.4	6.1	619	12	US-11-136-527-7645	Sequence 7645, Ap
11	36.2	6.1	1400	12	US-11-136-527-4371	Sequence 4371, Ap
12	36.2	6.1	3624	7	US-10-755-092-6	Sequence 6, Appli
13	36.2	6.1	4509	12	US-11-087-100-5	Sequence 5, Appli
14	36.2	6.1	4509	12	US-11-087-084-5	Sequence 5, Appli
15	36.2	6.1	4509	12	US-11-087-085-5	Sequence 5, Appli
16	36.2	6.1	5941	12	US-11-136-527-2775	Sequence 275, App
17	35.2	5.9	600	12	US-11-136-527-5577	Sequence 5577, Ap
18	35.2	5.9	658	12	US-11-136-527-1481	Sequence 1481, Ap
19	35.2	5.9	1488	12	US-11-219-995-3	Sequence 3, Appli
20	35.2	5.9	1642	6	US-09-923-055A-552370	Sequence 552370,

	Query Match	7.0%;	Score 41.6;	DB 12;	Length 1280;
	Best Local Similarity	52.%;	Pred. No. 0.044;		
	Matches 89;	Conservative	0;	Mismatches 80;	Indels 0; Gaps 0;
Qy	266	ACGCCCATCTGTGTC	AAGGGCCA	CGGCTGTGAC	CACCGCCCATCTTTGAC
Db	405	ACCTACCTCAGGGCAG	CGGGCTTCTG	CTCGTGGCCAGCTCA	ACCTTGGACACGCGCAGCT
Qy	326	ACCTTGGAGACGCTG	CAAGAGATGGG	CGCTCAAGCAGAGTGT	GCATCCAGCAGCGCCGCG
Db	465	CGCTTGGGGGAAAC	CGCGACGAAGATCG	CTTCGTCATCTCTGCT	CAGCAAGAGGCGCCGACG

PRIOR APPLICATION NUMBER: 09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/532,591
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/713,994
PRIOR FILING DATE: 2000-11-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 430
SOFTWARE: PatentIn version 3.2
SEQ ID NO 161
LENGTH: 859
TYPE: DNA
ORGANISM: *Triticum aestivum*
FEATURE:
OTHER INFORMATION: G3736 Predicted polypeptide sequence is orthologous to G1792
US-10-714-887-161

Query Match 6.2%; Score 37; DB 7; Length 859;
Best Local Similarity 50.6%; Pred. No. 0.83;
Matches 88; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 257 ACGACCCACACGCCCATCTGTCAAGGCGCCACCGCTGACACCCGCCACTTTGACAAGA 316
DB 350 ACCGGCGCACGCTACGAGGCGCGCCAGCGCCAGCGCGCCAGCGCTTCTGCTCGG 409
QY 317 TCAAGCAGTACCTTGCAGAGACGCTCAAGAGATGGCGGTCAAGCAGGATGTGATCCAGC 376
DB 410 CGAGGCGACAGATCAGCAGCAGCAGCAGGCGGAGCGGGGTGATCGAGTTCGAGTACC 469
QY 377 ACGCCCGCGAGTGGTGGAGTCCACCCGCGAGCAATTTGACTTNCACCAACT 430
DB 470 TGACGACGACGCTGCTGCAGTCCATGCTCCACGACCAACCAACTCAACACT 523

RESULT 5
US-11-136-527-3173
Sequence 3173, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3173
LENGTH: 1222
TYPE: DNA
ORGANISM: *Rattus norvegicus*
FEATURE:
NAME/KEY: misc feature
LOCATION: (673)..(673)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (802)..(802)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (910)..(910)
OTHER INFORMATION: n is a, c, g, or t

FEATURE:
NAME/KEY: misc feature
LOCATION: (912)..(912)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (925)..(925)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1063)..(1063)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1074)..(1074)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1077)..(1077)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1080)..(1080)
OTHER INFORMATION: n is a, c, g, or t
US-11-136-527-3173

Query Match 6.2%; Score 37; DB 12; Length 1222;
Best Local Similarity 50.3%; Pred. No. 0.89;
Matches 91; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 14 ACGCGCCACACGACACGAGAGCGGGAAGCGGATGCGGGCGCAAGAGCTGTTTG 73
DB 196 AGGAGGCGCTTCAACATGATTCAGAACCGTGCTTCATTGACAAGGAGGACCTAC 255
QY 74 ATGACTGGCGCGCCAGAGGACATGAGCTGCGGTTTCACACCTTCTACGATAAGGTGC 133
DB 256 ATGATGATGTCGCTCCCTCGGGGAAGAACCCACGATGAGTACCTGGAGGGTATGATGA 315
QY 134 TGGCTGACCGGAGCTGCTGCCCTTCTTCGAGTCCCTGACATGCAAGAGCAGAAGATGA 193
DB 316 ACGAGGCGCGGACCTATCACTTCACTATGTTTGGGGAAGCTGA 375
QY 194 A 194
DB 376 A 376

RESULT 6
US-11-069-834-49
Sequence 49, Application US/11069834
Publication No. US20050276811A1
GENERAL INFORMATION:
APPLICANT: CARROLL, MICHAEL C.
APPLICANT: MOORE JR., FRANCIS D.
APPLICANT: HECHTMAN, HERBERT B.
TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
FILE REFERENCE: CRA-002.01
CURRENT APPLICATION NUMBER: US/11/069,834
CURRENT FILING DATE: 2005-03-01
PRIOR APPLICATION NUMBER: 60/588,648
PRIOR FILING DATE: 2004-07-16
PRIOR APPLICATION NUMBER: 60/549,123
PRIOR FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 49
LENGTH: 7474
TYPE: DNA
ORGANISM: *Homo sapiens*
US-11-069-834-49
Query Match 6.2%; Score 36.8; DB 12; Length 7474;
Best Local Similarity 46.1%; Pred. No. 1.4;

Matches	165;	Conservative	0;	Mismatches	187;	Indels	6;	Gaps	1;
QY	65	AGCTGTTTGATGACCTGGGGCGGCAGAAAGCATGAAGCTGGCGGTTTGACACCTTCTTACG	124						
Db	4812	AGCTGGAGGACGAGCTGCAGGCCACCGAAGATGCAAGCTGCGGTTTGGAGGTCAACCTGC	4871						
QY	125	ATAAGGTGCTGCTGACCCGAGCTGTCGCCCTTCTTCGAGTCCCTGGACATGCACAGGC	184						
Db	4872	AGGCCATGAAGGCCCGAGTTTCGAGCGGACCTGCAGGGCCGGGACGAGCAGAGCGAGGAGA	4931						
QY	185	AGAAGATGAAGCAGGCTCAAGTTTCATGAGCTTTCGTGTTTGGCGGAGCAGACCAATACAAGG	244						
Db	4932	AGAAGAAGCAGCTGGTCAGACAGCTGCGGAGATGGAGGCGAGAGCTGGAGGACGAGAGGA	4991						
QY	245	GCCGAGATGTTAGAGCGACACGCCCATCTGGTCAAGGGCCAGGCTTGGACACC---	301						
Db	4992	AGCAGCGCTCGATGGCAGTGGCGGTCGCCGCCGAGAGCTTGGAGATGGACCTGAAGGACCTGG	5051						
QY	302	---GCCACTTTGACAAGCATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGGCGTCA	358						
Db	5052	AGSGGCACATCGACTCGGCCAACAGAACCGGGACGAGGCATCAACACGTGCGGNAAGC	5111						
QY	359	AGCAGGATGTGATCCAGCACGCCGCCGGAGTGTTGGAGTCAACCCGCGACGAATTGA	416						
Db	5112	TGCAGGCCCATGAAGGACTGTCATGCGCAGCTGGATGATCACCCGCGCTCTCGTGA	5169						

RESULT 7

US-11-136-527-2717

; Sequence 2717, Application US/11136527

; Publication No. US2005028750A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)

; CURRENT APPLICATION NUMBER: US/11/136,527

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294

; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2717

; LENGTH: 2644

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-11-136-527-2717

```

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 662231
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-662231

Query Match      6.1%; Score 36.4; DB 6; Length 581;
Best Local Similarity 47.7%; Pred. No. 1.1;
Matches 103; Conservative 1; Mismatches 112; Indels 0; Gaps 0;

Qy      178  CAAGAGCAGAGATGAAGCAGAGTCAAGTTCATCAGCTTCGTGTTGGCGGAGCAGACCAA 237
Db      251  CCAGCGCACCCGACGACGCGCCGCGAGCTCGTCGGGCCATGTTCCAGGCGGCCGAGCGC 192

Qy      238  TACAAGGGCGGAAGCATGTACGACGACACGCCCCATCTGGTCTAAGGCCACGGCCTTGGAC 297
Db      191  CCCACGAGTGGGCCATGGAGGGGCCCGCGAGCGGGCTGAAGAAGGAGCGGCTACTGGAY 132

Qy      298  CACGGCCACTTTTACAAGATCAAGCAGTACCTTTGGAGAGACGCTGCAAGAGATGGCGGTC 357
Db      131  GACCGCCACGACAGCGGCTGGACTCCATGAAGAAGAGAGATACGAGCAGATGCTCAAG 72

Qy      358  AAGCAGGATGTGATCCAGCAGCGCCGCGGAGTGGTG 393
Db      71  GAGCTGCAGGAGATCCGCTTCGAGCGCGCAGGAGTG 36

```

Db 11 GCCATGATGCGGAGGAGCTGAAGAGGAGCAGGACACGAGCCCATCTGGAGCGGATG 70
QY 232 GACCAATACAAAGGCGGAGCTGTACGAGCAGCAGCCCATCTGTCAAGGGCCACGGC 291
Db 71 AAGAAGAACCTGGAGCAGACAGTGAAGGACCTGCAGCACCGTCTGCAGGAGCTGAGCAG 130
QY 292 CTGGACACCGCCACCTTTGACAGATCAAGCAGTACCTTGGAGAGCGCTGCAAGAGATG 351
Db 131 CTGGCCCTGAAGGCTGCAAGAGCAGATCCAGAACTGAGGCCAGGGTGCGGGAGTTG 190
QY 352 GCGGTCAAGCAGGATGTGATCCAGCA 377
Db 191 GAAAGCGAGCTGGATGACAGAGCAGAA 216

RESULT 10

US-11-136-527-7645
; Sequence 7645, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7645
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-7645

Query Match 6.1%; Score 36.4; DB 12; Length 619;
Best Local Similarity 48.5%; Pred. No. 1.1;
Matches 100; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
QY 172 GACATGCAAGAGCAGAGAGTGAAGAGGAGTCAAGTTCATGAGCTTCGTGTTGGCGGAGCA 231
Db 11 GCCATGATGCGGAGGAGCTGAAGAGGAGCAGGACACGAGCCCATCTGGAGCGGATG 70
QY 232 GACCAATACAAAGGCGGAGCTGTACGAGCAGCAGCCCATCTGTCAAGGGCCACGGC 291
Db 71 AAGAAGAACCTGGAGCAGACAGTGAAGGACCTGCAGCACCGTCTGCAGGAGCTGAGCAG 130
QY 292 CTGGACACCGCCACCTTTGACAGATCAAGCAGTACCTTGGAGAGCGCTGCAAGAGATG 351
Db 131 CTGGCCCTGAAGGCTGCAAGAGCAGATCCAGAACTGAGGCCAGGGTGCGGGAGTTG 190
QY 352 GCGGTCAAGCAGGATGTGATCCAGCA 377
Db 191 GAAAGCGAGCTGGATGACAGAGCAGAA 216

RESULT 11

US-11-136-527-4371
; Sequence 4371, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4371

; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4371
Query Match 6.1%; Score 36.2; DB 12; Length 1400;
Best Local Similarity 40.4%; Pred. No. 1.5;
Matches 86; Conservative 22; Mismatches 105; Indels 0; Gaps 0;
QY 169 CTGGCATGCAAGAGCAGAGTGAAGCAGAGTCAAGTTCATGAGCTTCGTGTTGGCGGA 228
Db 15 CTGGGKCAASKGGGAARARYRTSCAGAGCTGGAGAGRTCCKMWRGCMWYTKGWSGW 74
QY 229 GCAGACCATAACAAGGGCCGGAAGCATGTACGAGGACACAGCCCATCTGTCAAGGGCCAC 288
Db 75 GRGMMGCKSRGCGYCGAGTCAGCCCTTGAAGAGGCTGAGGCCCTCYCTGGAGCATGAGGAG 134
QY 289 GGCCTGGACACCGCCACCTTTGACAGATCAAGAGTCAAGCAGTACCTTGGAGAGAGCGCTGCAAGAG 348
Db 135 GCAAGATCTCCGAGCCAGCTGGAGTTCAACCATYAAAGCAGAGATCGAAGAG 194
QY 349 ATGGGCGTCAAGCAGGATGTGATCCAGCAGGCC 381
Db 195 CTGGCAGAGAARGACGAGGAGATGGAGCARGSC 227

RESULT 12

US-10-755-092-6
; Sequence 6, Application US/10755092
; Publication No. US20060021095A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/755,092
FILING DATE: 08-Jan-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-Nov-2001
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy

```
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-188051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3624 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHEetical: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3621
; OTHER INFORMATION: /product= "Full-length, maize
; optimized cry1B"
; /note= "Disclosed in Figure 6."
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
US-10-755-092-6

Query Match 6.1%; Score 36.2; DB 7; Length 3624;
Best Local Similarity 44.4%; Pred. No. 1.9;
Matches 146; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 78 CTTGGGGCGGCGAAGGATGAAGCTGGGGTGTGACACTTCTACGATAGGTGCTGGC 137
Db 2811 CGTGGACAGCGAGTACGACCGCTCGAGCGCGACCAACATCGGCATGATCCACGCCG 2870

QY 138 TGACCGGAGCTGCTGCCCTTCTCGAGTCCCTGGACATCAAGAGCAGAGATGAAGCA 197
Db 2871 CGAAGCTGGTGACCGCATCCGAGGCTTCTGAGGAGCTGCCCTGTATCCCGG 2930

QY 198 GGTCAAGTTTCATGAGTCTGTTTGGCGGAGCAGCAATCAAGGGCGCGAAGCATGTA 257
Db 2931 CGTGAAGCGCGAGATCTTCGAGGAGCTGGAGGCGCATCATCACCGCCATCAGCTGTA 2990

QY 258 CGACGACACGCCCATCTGTGAAGGCGCCACGGCTGGACACCGCCACTTTGACAGAT 317
Db 2991 CGACGCCGCAACGTGGTGAAGAACGGCGACTTCAACACGGGCTGACCTGTGGAACGT 3050

QY 318 CAAGCAGTACTTGGAGAGCGCTGCAAGATGGGCTCAAGCAGATGTGATCCAGCA 377
Db 3051 GAAGGGCCAGCTGACGTGAGCAGAGAGCCACCGCAGCGACCTGGTGATCCCGGAGT 3110

QY 378 CGCGCGCGAGTGGTGAGTCCACCGCG 406
Db 3111 GGAGGCGGAGGTGAGCCAGGCGGTGGCGG 3139

RESULT 13
US-11-087-100-5
; Sequence 5, Application US/11087100
; Publication No. US2005026640A1
; GENERAL INFORMATION:
; APPLICANT: Metz, James
; APPLICANT: Barclay, William
; APPLICANT: Platt, James
; APPLICANT: Kuner, Jerry
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
; FILE REFERENCE: 2997-29
; CURRENT FILING DATE: 2005-03-21
; PRIOR APPLICATION NUMBER: 09/231,899
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 60/284,066
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/298,796
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/323,269
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5
; LENGTH: 4509
; TYPE: DNA
; ORGANISM: Schizochytrium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4509)
; US-11-087-084-5

Query Match 6.1%; Score 36.2; DB 12; Length 4509;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 89; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 266 ACGCCCATCTGGTCAAGGGCCACGGCTGGACCAACCGCCACTTTGACAAGATCAAGCAGT 325
Db 1070 ACGGCCACCCCAACAAGGTCCGCTGCGCGGCCAAATCTCCCGCACAAAGGGAAGCTCG 1129

QY 326 ACCTTGGAGAGAGCTGCAAGAGATGGGCGTCAAGAGATGTGATCCAGACGCCCGCG 385
Db 1130 TCTACGTCATGGAGATCAAGGAGATGGGCTTCGACGAGCAACAGACCCCTAGCCATTG 1189

QY 386 GAGTGTGGAGTCCACCGCGACGAAATTTGACTTNCACCACTGGCACCACCACTG 443
Db 1190 CCGACGTCACATCATTTGATGTCGACTTCGAAAAGGCGCAGGACTTTAGCTCGACCG 1247
```

```
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5
; LENGTH: 4509
; TYPE: DNA
; ORGANISM: Schizochytrium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4509)
; US-11-087-100-5

Query Match 6.1%; Score 36.2; DB 12; Length 4509;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 89; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 266 ACGCCCATCTGGTCAAGGGCCACGGCTGGACCAACCGCCACTTTGACAAGATCAAGCAGT 325
Db 1070 ACGGCCACCCCAACAAGGTCCGCTGCGCGGCCAAATCTCCCGCACAAAGGGAAGCTCG 1129

QY 326 ACCTTGGAGAGAGCTGCAAGAGATGGGCGTCAAGAGATGTGATCCAGACGCCCGCG 385
Db 1130 TCTACGTCATGGAGATCAAGGAGATGGGCTTCGACGAGCAACAGACCCCTAGCCATTG 1189

QY 386 GAGTGTGGAGTCCACCGCGACGAAATTTGACTTNCACCACTGGCACCACCACTG 443
Db 1190 CCGACGTCACATCATTTGATGTCGACTTCGAAAAGGCGCAGGACTTTAGCTCGACCG 1247

RESULT 14
US-11-087-084-5
; Sequence 5, Application US/11087084
; Publication No. US20050273883A1
; GENERAL INFORMATION:
; APPLICANT: Metz, James
; APPLICANT: Barclay, William
; APPLICANT: Platt, James
; APPLICANT: Kuner, Jerry
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
; FILE REFERENCE: 2997-29
; CURRENT FILING DATE: 2005-03-21
; PRIOR APPLICATION NUMBER: US/11/087,084
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 09/231,899
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/284,066
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/298,796
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/323,269
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5
; LENGTH: 4509
; TYPE: DNA
; ORGANISM: Schizochytrium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4509)
; US-11-087-084-5

Query Match 6.1%; Score 36.2; DB 12; Length 4509;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 89; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 266 ACGCCCATCTGGTCAAGGGCCACGGCTGGACCAACCGCCACTTTGACAAGATCAAGCAGT 325
Db 1070 ACGGCCACCCCAACAAGGTCCGCTGCGCGGCCAAATCTCCCGCACAAAGGGAAGCTCG 1129

QY 326 ACCTTGGAGAGAGCTGCAAGAGATGGGCGTCAAGAGATGTGATCCAGACGCCCGCG 385
Db 1130 TCTACGTCATGGAGATCAAGGAGATGGGCTTCGACGAGCAACAGACCCCTAGCCATTG 1189
```

QY 386 GAGTGTGAGTCCACCCGCGACGAATTGACTTNCCTCCAACTCCGCGACCCCACTG 443
Db 1190 CCGACGTCAACATCATGTGCTGACTTCGAAAAGGCCAGGACTTTAGCTCGACCG 1247

RESULT 15

US-11-087-085-5
; Sequence 5, Application US/11087085
; Publication No. US20050273884A1
; GENERAL INFORMATION:
; APPLICANT: Metz, James
; APPLICANT: Barclay, William
; APPLICANT: Platt, James
; APPLICANT: Kuner, Jerry
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORPA of a PUFA Polyketide Synthase
; FILE OF INVENTION: System and Uses Thereof
; FILE REFERENCE: 2997-29
; CURRENT APPLICATION NUMBER: US/11/087,085
; CURRENT FILING DATE: 2005-03-21
; PRIOR APPLICATION NUMBER: 09/231,899
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 60/284,066
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/298,796
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/323,269
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 4509
; TYPE: DNA
; ORGANISM: Schizochytrium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4509)
US-11-087-085-5

Query Match 6.1%; Score 36.2; DB 12; Length 4509;
Best Local Similarity 50.0%; Pred.No. 1.9;
Matches 89; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY 266 AGCCCATCTGTCAAGGCGCCAGCGCTGGACCCACCGCCACTTTGACAAGATCAAGCACT 325
Db 1070 ACGGCCACCCACAAAGGTCGGTCGCGGGCCAAATCTCCCGCACAAAGGGCAAGCTCG 1129
QY 326 ACCTTGGAGAGCGCTGCAAGAGATGGCGTCAAGCAGATGTGATCCAGCAGCGCCCG 385
Db 1130 TCTACGTCATGAGATCAAGGAGATGGGCTTCGACGAGGACAAACGACCGGTACGCCATTG 1189
QY 386 GAGTGTGAGTCCACCCGCGAGATTGACTTNCCTCCAACTCCGCGACCCCACTG 443
Db 1190 CCGACGTCAACATCATGTGCTGACTTCGAAAAGGCCAGGACTTTAGCTCGACCG 1247

Search completed: February 27, 2006, 20:30:24
Job time : 432 secs

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 19:14:39 ; Search time 171 Seconds
(without alignments)
6216.268 Million cell updates/sec

Title: US-09-920-953-2
Perfect score: 597
Sequence: 1 GCGCTGCTGCGAGCGGCG.....AGCCATTTTCGACCAAGCG 598

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/6H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97.2	16.3	381	3	US-09-902-540-5776
2	97.2	16.3	72704	3	US-09-902-540-1273
C 3	46.4	7.8	4403765	3	US-09-103-840A-2
C 4	46.4	7.8	4411529	3	US-09-103-840A-1
5	45.2	7.6	1143	3	US-09-902-540-8600
6	45.2	7.6	6821	3	US-09-902-540-907
C 7	43.4	7.3	603	3	US-09-902-540-14
8	43.4	7.3	603	3	US-09-902-540-5853
9	42.8	7.2	585	3	US-09-902-540-3555
10	42.8	7.2	19019	3	US-09-902-540-1171
11	42.6	7.1	3128	3	US-09-744-072-1
12	42.4	7.1	26896	3	US-09-949-016-16800
13	42.2	7.1	759	3	US-09-252-991A-11092
14	42	7.0	1058	3	US-09-452-239-11
15	41.6	7.0	969	3	US-09-902-540-8164
16	41.6	7.0	1280	3	US-09-096-776B-4
17	41.6	7.0	1280	3	US-09-923-922-4
18	41.6	7.0	1491	3	US-09-082-092-9
19	41.6	7.0	1491	3	US-09-885-722A-9
20	41.6	7.0	1524	3	US-08-840-767-3
21	41.6	7.0	1817	3	US-09-288-292A-45
22	41.6	7.0	2887	3	US-09-679-298A-1
23	41.6	7.0	3083	2	US-08-480-994-36
24	41.6	7.0	3083	2	US-08-616-844-36

ALIGNMENTS

RESULT 1
US-09-902-540-5776
; Sequence 5776, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5776
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5776

Query Match	16.3%;	Score 97.2;	DB 3;	Length 381;
Best Local Similarity	56.9%;	Pred. No. 9.8e-16;		
Matches 199;	Conservative	0;	Mismatches 148;	Indels 3; Gaps 1;
QY	61	AGAGAGCTGTTTGATGACCTGGCGCGCAGAGGATGAACTGGCGGTTCACACCTTC	120	
DB	19	AGAGGTGTCTACGAGCAGCTGGCGCGGAGAGCGCGCATGGCGCGGTGGAGGTCTTC	78	
QY	121	TACGATAAGTCTGGCTGACCGCGAGCTGTGCCCTTCTTCGAGTCCCTGGACATGCAA	180	
DB	79	TACCGAGGTCTGGCGGACGATCATCACCACCTTCTTCGAGGACGTGGACATGGAG	138	
QY	181	GAGCAGAGATGAAGCAGGTCAAGTTCATGAGCTTCGTGTTGGCGGAGCAGACCAATAC	240	
DB	139	CGCCAGGCGCGAAGCAGAGCGTTCCTGACGATGTTGACGGTGGCGGTCCACTAC	198	
QY	241	AAGGGCGGAGCATGTACGACCAACGGCCATCTGGTCAAGGGCCACGGCTTGGACCA	300	
DB	199	TCGGGCAAGGACATCGCGCGGCCACCGCTCTCTGGTGAAG---CGTGGGTGAAACGAC	255	
QY	301	CGCCACTTTGACAAAGATCAAGCAGTACCTTGGAGAGACGCTCAAGAGATGGCGCTCAAG	360	
DB	256	TGCACCTTCGACCGGTGGCGGGCCACCTGAAGGGCAGCGCTGGAGGAGCTGGCGGTGGCC	315	
QY	361	CAGGATGTGATCCAGCAGCGCCCGGAGTGGTGGAGTCCACC CGCGGACGA	410	

Db

RESULT 2

```

US-09-902-540-1273
; Sequence 1273, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Ge
; FILE REFERENCE: 38-10(15949)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1273
; LENGTH: 72704
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72704)
; OTHER INFORMATION: unsure at all n locat
US-09-902-540-1273

```

Query Match 16.3%; Score 97.2; DB 3; Length 72704;
Best Local Similarity 56.9%; Pred. No. 4.6e-15;
Matches 199; Conservative 0; Mismatches 148; Indels 3; Gaps 1;
Qy 61 AAGAAGGTGTTTATGACCTTGGCGCGCGAGGCATGAAGCTGCGGTTGACACCTTC 120
Db - 21785 AAGAGTGTCTACAGACAGCTGGCGCAGAGCCGGCATGGCGCGCGCTGTGAGGTCCTC 21844

Qy	121	TACGATAAGG	TGCTGCTGAC	CCGGAGCTG	TGCTCCCTTCTTCG	AGTCCCTGGAC	ATGCAA	180
Db	21845	TACCGAAGG	TGCTGCGAC	GATCATCATCAG	CCACTTCTTCG	AGGACGTGGAC	ATGGAG	21904
Qy	181	GACGAGAAG	GATGAAGCAG	GTCAAGTT	CATGAGTTCG	TGTTGGCGG	AGCAGACCAATAC	240
Db	21905	CGCCAGCG	CGGACGAAAG	GCGTTCCTGA	CGATGCTGAC	GCGGTGGCG	CGGTCCACTAC	21964
Qy	241	AAGGGCCG	AAGCATGTAC	GACGCGAC	CACGGCCCATCTTG	TGTCAGGGG	CCACGGCTTGAGCCAC	300
Db	21965	TCGGGCAAG	GACATGCGCG	CGGCCACGGCC	CTCTGTTGTAAG	---CGTGGG	CTGTAACGAC	22021
Qy	301	CGCCACTTT	TGACAAGATCA	AGCAGTAGTAC	CTTTGGAGAGAC	CGCTCCAAGAGAT	TGGCGCTCAAG	360
Db	22022	TCCCACTT	CGACCGGTGG	CGGGCCACTTGA	AGGCGACCTCGAG	AGGACTTGGG	CGTGGCC	22081
Qy	361	CAGGATGT	GATCCAGCAC	CGCCCGGAGT	TGGTGGATCC	ACCCGCGAC	GAA	410
Db	22082	GCSCCG	CTGTGCGGAG	GGTGATGAC	CACTCGCGGAG	CGCCCGCGGAG	22131	

RESIT.T 3

```

RESOL 3
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24

```

```

; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765

```

Query Match	7.8%;	Score 46.4;	DB 3;	Length 4403765;
Best Local Similarity	50.9%;	Pred. No. 0.23;		
Matches 110;	Conservative	0;	Mismatches 106;	Indels 0; Gaps 0;
Qy	51	ATCGGGCGCGCAAGAAGCTGTTTGATCACCTGGGCGCGCGAGAGGCATGAAGTCGCGGT	110	
Db	1744933	ACGTGAGCCGATCAGCATCTACGACAAGATCGCGGGCATGAGCCATCGAAGTCGTCGT	1744874	
Qy	111	TGACACCTTTCTACGATAAAGTGTGTGCTGACCCGGAGCTGTGTCCTCTTCTCGAGTCCCT	170	
Db	1744873	CGAGGACTTCTATGTGTTCTGTGTCTGCCGATGACCAACTATCGGCGCTTCTTCACGCGGTAC	1744814	
Qy	171	GGACATGCAAGCAGCAGAAGATGAAGCAGGTCAAAGTTTCATGAGCTTCGTGTGTTTCGGCGGAGC	230	
Db	1744813	GAACATGAGCGCCCTCAAGGCGAAGCAGGTGGAGTGTTCGGGCGCGCTTCGGCGGCC	1744754	
Qy	231	AGACCAATCAAGGGCGCGAAGCATGTACGACGCACA	266	
Db	1744753	CGAGCCCTATACCGGTGCGCCGATGAAGCAAGTCCA	1744718	

RESULT 4

```

US-09-103-840A-1/c
? Sequence 1, Application US/09103840A
? Patent No. 6294328
? GENERAL INFORMATION:
? APPLICANT: FLEISCHMAN, Robert D.
? APPLICANT: WHITE, Owen R.
? APPLICANT: FRASER, Claire M.
? APPLICANT: VENTER, John C.
? TITLE OF INVENTION: DNA SEQUENCES FOR STRA
? TITLE OF INVENTION: TUBERCULOSIS
? FILE REFERENCE: 24366-20007.00
? CURRENT APPLICATION NUMBER: US/09/103,840A
? CURRENT FILING DATE: 1998-06-24
? NUMBER OF SEQ ID NOS: 2
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 1
? LENGTH: 4411529
? TYPE: DNA
? ORGANISM: Mycobacterium tuberculosis
? OTHER INFORMATION: H37Rv
US-09-103-840A-1

```

Query Match	7.8%;	Score 46.4;	DB 3;	Length 4411529;
Best Local Similarity	50.9%;	Pred. No. 0.23;		
Matches 110;	Conservative 0;	Mismatches 106;	Indels 0;	Gaps 0;
QY	51	ATGCGGCGCAAGAAGCTGTTTCATGACCTGGCGCGCAAGAGGATGAAGCTGGCGGT	110	
Db	1744808	ACGTGAGCCGATCAGCATCTACGACACAGATCGCGGGCATGAGCCATCGAAGTGTGTCGT	1744749	
QY	111	TGACACCTTCTACGATAAGTGTGGCTGACCCGCGAGCTGCTGCCCTTCTTCGAGTCCCT	170	
Db	1744748	CGAGGACTTCTATGTTTCGTGTGCTGCCGATGACCAACTATCGGCCCTTCTTCACGCGGTAC	1744689	
QY	171	GGACATCGACAGACGAGATGAAGCAGGTCAGTTTCATGAGCTTCGTGTTTCGCGCGAGC	230	
Db	1744688	GAACATGAGCGCGCTCAAGGCGCAAGCAGGTGGAGTTTTTCGCGCGCGCGCTTGGCGGGCC	1744629	
QY	231	AGACCAATACAAGGGCGCGAAGCATGTACGACGCACA	266	

Db 1744628 CGAGCCCTATACCGGTGCGCGGATGAAGCAAGTCCA 1744593

RESULT 5

US-09-902-540-8600
; Sequence 8600, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 8600

; LENGTH: 1143

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

US-09-902-540-8600

Query Match 7.6%; Score 45.2; DB 3; Length 1143;
Best Local Similarity 45.5%; Pred. No. 0.04;

Matches 158; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 82 GCGGGCGGAGAGGATGAAGCTGGCGGTGACACCTTCTACGATGAAGTGTGGCTGAC 141

Db 169 GGGCTCGCTCGCGCGAGGCGCTGGCGGACGTGCTTCTCCAGACAGCGGCTGTCAAGC 228

QY 142 CCGGAGCTGTGCTCTTCTCGAGTCCCTGCGATCAAGAGCAGAGATGAAGCAGGTC 201

Db 229 TCGGGACCGGTGTCTCGCGAGCTGCCATGCGGCGAGGCTGACGCTGCCACCGCC 288

QY 202 AAGTTTCATGAGCTTCGTGTTGGCGAGCAGACCAATACAGGGCGGCGAAGCATGTACGAC 261

Db 289 AAGGCCAAGGCTGCGACGACACCTGTCCGAGCGCAACCGCCACCTGCTGAACGTG 348

QY 262 GCACAGCCCATCTGTGTGAAGGCGCACGGCTGGACACCGCCACTTTGACAGATCAAG 321

Db 349 GCGTCAACACCGGTGTCTATGTGGACGACGCGGCGGCGGCTCTGGAACAGGCGCATC 408

QY 322 CAGTACCTTGGAGAGACGCTGCAAGAGATGGGGTCAAGCAGATGTGATCCAGCAGCC 381

Db 409 CTGCGCGCTGCTCAACCGGTGGAGATGAACGCGGACGCGAGTGTGGCGCCCGGCTC 468

QY 382 GCGGAGTGTGGAGTCCACCGCGACGAATTTGACTTNCACAA 428

Db 469 ACCTCGGTGGATCGTACACCGAGTACCGAGTACCGAGGCTCTTCGGCAA 515

RESULT 6

US-09-902-540-907

; Sequence 907, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 907

; LENGTH: 6821

US-09-902-540-907

Query Match 7.3%; Score 43.4; DB 3; Length 603;

Best Local Similarity 45.4%; Pred. No. 0.097;

Matches 152; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 30 CACAGAGCGCGGAGCGGATGCGGGCGGCGAAGAGTGTGATGACCTGGCGGCGC 89

Db 601 CGCAATCCCCGNCGTGGTGGGCGTGACNCGCGTGGTGGTGGCCACCTGACGCTGT 542

QY 90 AGAAGCATGAAGCTGGCGGTGACACCTTCTACATGAAGTGTGGCTGACCCCGAGCT 149

; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(6821)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-907

Query Match

Best Local Similarity 45.5%; Score 45.2; DB 3; Length 6821;

Matches 158; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 82 GCGGGCGGAGAGGATGAAGCTGGCGGTGACACCTTCTACGATGAAGTGTGGCTGAC 141

Db 5097 GGGCTCGCTCGCGCGAGGCGCTGGCGGACGTGCTTCTCCAGACAGCGGCTGTCAAGC 5156

QY 142 CCGGAGCTGTGCTCTTCTCGAGTCCCTGCGATCAAGAGCAGAGATGAAGCAGGTC 201

Db 5157 TCGGGACCGGTGTCTTCTCGCGAGCTGCCATGCGGCGGAGGCTGACGCTGCCACCGCC 5216

QY 202 AAGTTTCATGAGCTTCGTGTTGGCGAGCAGACCAATACAGGGCGGCGAAGCATGTACGAC 261

Db 5217 AAGGCCAAGGCTGCGACGACACCTGTCCGAGCGCAACCGCCACCTGCTGAACGTG 5276

QY 262 GCACAGCCCATCTGTGTGAAGGCGCACGGCTGGACCAACCGCCACTTTGACAGATCAAG 321

Db 5277 GCGTCAACACCGGTGTCTATGTGGACGACGCGGCGGACCGGCTCTGGAACAGGCGCATC 5336

QY 322 CAGTACCTTGGAGAGACGCTGCAAGAGATGGGGTCAAGCAGATGTGATCCAGCAGCC 381

Db 5337 CTGCGCGCTGCTCAACCGGTGGAGATGAACGCGGACGCGAGTGTGGCGCCCGGCTC 5396

QY 382 GCGGAGTGTGGAGTCCACCGCGACGAATTTGACTTNCACAA 428

Db 5397 ACCTCGGTGGATCGTACACCGAGTACCGAGTACCGAGGCTCTTCGGCAA 5443

RESULT 7

US-09-902-540-14/c

; Sequence 14, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 14

; LENGTH: 603

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(603)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-14

Query Match

Best Local Similarity 45.4%; Score 43.4; DB 3; Length 603;

Matches 152; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 30 CACAGAGCGCGGAGCGGATGCGGGCGGCGAAGAGTGTGATGACCTGGCGGCGC 89

Db 601 CGCAATCCCCGNCGTGGTGGGCGTGACNCGCGTGGTGGTGGCCACCTGACGCTGT 542

QY 90 AGAAGCATGAAGCTGGCGGTGACACCTTCTACATGAAGTGTGGCTGACCCCGAGCT 149

Db 541 GCTCAACCCGCGAGTGCTCAACGACCCCGCGGCGCCGCAAGGTGTCTCGGCACTC 482
QY 150 GCTGCGCCCTTCTGAGTCCCTGGACATGCAAGACGAGCAAGATGAAGCAGGTCAAGTTTCA 209
Db 481 TGGCGCTTCCCAAGTACGTGGCGCGCTGGAGCTGGTGTGAAGATGCCGAGGTGCT 422
QY 210 GAGCTTTGCTTTTGGCGGAGCAGACCAATACAAGGCGCGGAGCATGTACGACGCAACGC 269
Db 421 CGGCACCGGTGAGGCGCGGAAATCATCAGCCAGGACTACCGCGGTGTTCCTCCATGACGCG 362
QY 270 CCATCTGCTCAAGGCGCACCGCTGGACACCGCCACTTTTGACAAGATCAAGCAGTACCT 329
Db 361 CCTGTGTGCGAGACGCCATGCGCGCTTCCGCCACGACACACGCGGTGTCTTGGGAGGA 302
QY 330 TGGAGAGACGCTGCAAGAGATGGCGTCAAGCAGG 364
Db 301 GGGCCAGTTCTCGGACGAGCGAGTCCGTGAGG 267

RESULT 8

US-09-902-540-5853
; Sequence 5853, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5853
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(603)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-5853

Query Match 7.3%; Score 43.4; DB 3; Length 603;
Best Local Similarity 45.4%; Pred. No. 0.097;
Matches 152; Conservative 0; Mismatches 183; Indels 0; Gaps 0;
QY 30 CACAGAGACGCGCAAGCGGATCGGCGCGCAAGACTGTTTGATGACCTGGCGCGCGC 89
Db 3 CGCAAAATCCCGGNCGTGTGGCGGTGGACNCGGTGATGGTGGCCACCTGCACGTGCT 62
QY 90 AGAAGGCATGAAGCTGGCGGTGTGACACTTTCTACGATAAGTGTGCTGACCCGCGAGCT 149
Db 63 GCTCAACCGCGCGAGTGTCTACCGACCCCGCGCGCAAGTGTGTGCTGCGGCACTC 122
QY 150 GCTGCGCTTCTGAGTCCCTGGACATGCAAGACGAGCAAGATGAAGCAGGTCAAGTTTCA 209
Db 123 TGGCGCTTCTCCCAAGTACGTGGCGCGCTGGAGCTGTGTGTAAGATGTCGCCGAGGTGCT 182
QY 210 GAGCTTGTGTTTGGCGGAGCAGACCAATACAAGGCGCGGAGCATGTACGACGCGCACACGC 269
Db 183 CGGCACCGGTGAGGCGCGGAAATCATCAGCCAGACTACCGCGTGTTCCTCCATGGAGCG 242
QY 270 CCATCTGCTCAAGGCGCCACCGCTTGGACACCGCCACTTTTGACAAGATCAAGCAGTACCT 329
Db 243 CCTGTGTGCGACGCGCATGCGCGCTTCCGCCACGACACACGCGTGTCTTGGGAGGA 302
QY 330 TGGAGAGACGCTGCAAGAGATGGCGGTCAAGCAGG 364
Db 303 GGGCCAGTTCTCGGCGACGAGCGAGTCCGTGAGG 337

RESULT 9

US-09-902-540-3555
; Sequence 3555, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3555
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3555

Query Match 7.2%; Score 42.8; DB 3; Length 585;
Best Local Similarity 48.4%; Pred. No. 0.14;
Matches 119; Conservative 0; Mismatches 127; Indels 0; Gaps 0;
QY 78 CCTGGCGCGCGCAGAGGCGATGAAGCTGGCGGTGTGACCTTCTACGATAAGGTGCTGGC 137
Db 18 CGTGGCGATCGCGGGCTGCTCCACCTGGGAGCGGTCTTCTTCGAGCGGATGCCAG 77
QY 138 TGACCCGCGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATGCAAGACGAGCAAGATGAAGCA 197
Db 78 CCAGGCGCAGATGCTGCGGAGCATCGAGAAGCTGGACAGAAGAGGAGCGCCAGACCAA 137
QY 198 GGTCAAGTTCATGAGCTTCTGTTGGCGGAGCAGACCAATACAAGGCGCGAAGCATGTA 257
Db 138 GGCCTGCATCAGCAAGTGGGAGAGCGCGCGGGGACCCCGGAGGACAGCTACGATTG 197
QY 258 CGAGCGCACACGCCCATCTGTCGAAGGCGCACCGCTGGACCCGCTTTCGACAAGAT 317
Db 198 CTCCTGCGGAGCAGTGTGGTGGTGGAGCGGCTGCGACGACCCCACTCCCGCGTCGAGAGCT 257
QY 318 CAAGCA 323
Db 258 CAAGCA 263

RESULT 10

US-09-902-540-1171
; Sequence 1171, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1171
; LENGTH: 19019
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(19019)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1171

Query Match 7.2%; Score 42.8; DB 3; Length 19019;
Best Local Similarity 48.4%; Pred. No. 0.39;
Matches 119; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 78 CTTGGCGCGGCAAGAGGATGAAGCTGGCGTTGACACCTTCTACGATAAGTGCTGGC 137
DB 9777 CGTGGCCATCGCGGGGCTGCTCACTGGAGACGGCTCTTCTTCGAGCGGATGCCAG 9836

QY 138 TGACCCGGAGCTGCTGCCCTTCTTCAGTCCCTGGACATGCAAGAGCAGAAGATGAAGCA 197
DB 9837 CCAGGCGCAGATGCTGGCGAGCATCGAAGCTGGACAAGAGGAGGCCAGCAGACCAA 9896

QY 198 GGTCAAGTTTCATGAGCTTCTGTTTGGCGGAGCAGACCAATACAAAGGCGCGAAGCATGTA 257
DB 9897 GGCCTGCATCAGCAAGTGGCGAAGCGCGCGGGGACCCCGGAGGACAGCTTACGATTG 9956

QY 258 CGAGGCACACGCCCATCTGTTCAAGGGCCACCGCTGGACCCAGCCCATTTGACAAAGAT 317
DB 9957 CTCCTGCGGGAGAGTGATGGCTGGCGACGACCCCAACCTCCCGCGTGGAGAAAGCT 10016

QY 318 CAAGCA 323
DB 10017 CAAGCA 10022

RESULT 11
US-09-744-072-1
; Sequence 1, Application US/09744072
; Patent No. 6825328
; GENERAL INFORMATION:
; APPLICANT: SCHERER, STEPHEN W.
; APPLICANT: MINASSIAN, BERGE A.
; APPLICANT: ROULEAU, GUY
; APPLICANT: DALGADO-ESCUETA, ANTONIO
; TITLE OF INVENTION: LAFORA'S DISEASE GENE
; FILE REFERENCE: 086671/0113
; CURRENT APPLICATION NUMBER: US/09/744,072
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/093,495
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: 60/130,269
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3128
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match 7.1%; Score 42.6; DB 3; Length 3128;
Best Local Similarity 50.7%; Pred. No. 0.26;
Matches 102; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1 GCCTGCTGTCAGACGCGGCCACAGCACCACAGACGCGCGAAGCGGATCGGGCGC 60
DB 22 GTGTGTCACCCCGCGTGGCGCGCGCGCGAGCTGCTGTGTGGTGGCGGCC 81

QY 61 AGAAGCTGTTTATACCTTGGCGCGCGCGAGAGGATGAGCTGGGGTTGACCTTC 120
DB 82 GAGCTGGGGGCTTGGAGCGCGCGGTGCGCTCGCTGAGGCGCGCGCACCGCGGG 141

QY 121 TAGATAAGTGTGCTGACCGCGAGCTGCTCCCTTCTTCAGTCCCTGGACATGCAA 180
DB 142 GCGAGCGGGCCCTTCGCTGCGAGGACCGGGCTGTGGCTCGGGAGGTGGAGCTGGCG 201

QY 181 GAGCAGAAAGATGAAGCAGGTTC 201
DB 202 GCCGAGGAGCGCGCGCAGGAC 222

RESULT 12

US-09-949-016-16800

; Sequence 16800, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16800
; LENGTH: 26896
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16800

Query Match

7.1%; Score 42.4; DB 3; Length 26896;

Best Local Similarity 47.7%; Pred. No. 0.55;
Matches 124; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 137 CTGACCCGGAGCTGTCGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAAGATGAAGC 196

DB 22334 CAGACCATGTGCCACTCTCTCTGACACAGCGGCCCATGATGGCAGAGGAGTGAAGA 22393

QY 197 AGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAAAGGCCGCAAGCATGT 256

DB 22394 AGGAGCAGGACACCAGCGCCACCTTGGAGCGCATGAAGAAGAACATGGAACAGACCATTA 22453

QY 257 ACAGCGCACACGCCCATCTGTTCAAGGGCCAGCGGCTGACACCCGCCACTTTGACAAGA 316

DB 22454 AGGACCTGCGAGCACCAGCGGTGGAGCGAAGCGGACAGCATGCCCTCAAGGCGCGCAAGAGC 22513

QY 317 TCAAGCAGTACTTGGAGAGACGCTGCAAGAGATGGCGTCAAGCAGAGGATGTGATCCAGC 376

DB 22514 AGCTGCAGAGCTGGAAGCGCGGTGCGGAGCTGGAGATGAGCTGGAGGCGGAGCAGA 22573

QY 377 ACGCCCGCGGAGTGGTGAG 396

DB 22574 AGCGCAAGCAGAGTCGGTG 22593

RESULT 13

US-09-252-991A-11092

; Sequence 11092, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 11092

; LENGTH: 759

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-11092

Query Match

7.1%; Score 42.2; DB 3; Length 759;

Best Local Similarity 51.9%; Pred. No. 0.21;

Matches	95;	Conservative	0;	Mismatches	88;	Indels	0;	Gaps	0;
Qy	53	GC	GGGCGCAAGAGCTGTTT	GATGACCTTGGCGCGCAGAGGCATGAA	GCTGCGCGTTG	112			
Db	500	GC	GACCGCAAGTGCTGGCCGCGGAGGGCGAGCGTGCCGACGCCTACCTCGCGGGTA	559					
Qy	113	AC	ACCTTCTACGATAAGGTGCTGGCTGACCGGAGCTGCTGCCCTTCTT	CGAGTCCCTGG	172				
Db	560	CC	GCTCGCTGGGACGGGAGCTGGGTACTTTCGACCTCGCAACGAGCTTTC	CGGCGCTGC	619				
Qy	173	AC	ATGCAAGAGCAGAAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTTGTTGGCGGAGCAG	232					
Db	620	AT	CGACACTGGAGAGCTGGAGCAGACCCGGCGGTGGCTTCGCCCATCGCATCGAGG	679					
Qy	233	ACC	235						
Db	680	ATC	682						

```

RESULT 14
US-09-452-239-11
; Sequence 11, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 1058
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-452-239-11

```

	Query Match	7.0%;	Score 42;	DB 3;	Length 1058;
	Best Local Similarity	52.9%;	Pred. No. 0.27;		
	Matches 90;	Conservative 0;	Mismatches 80;	Indels 0;	Gaps 0;
Qy	162	CGAGTCCCTCGACATGCAAGACGACAGATCAAGCAGCTCAAGTTCATGAGCTTCGTGTT	221		
Db	619	CAACTACTCTCAACTTACCACGAGCGCTGATGAAGCTGCTCAAGGTCGGCGGCGCTCGTCGG	678		
Qy	222	TGGCGGAGCAGACCAATCAAGGGCCGAAAGCATGTACGACGCACACAGCCCATCTGGTCAA	281		
Db	679	CTACGACACACAGCTCTGGACGGCTCCGTGTCCTCCCGCGACGCCCATGGCAA	738		
Qy	282	GGGCCACGGCTCGGACCAACGCCCACTTTGACAAGATCAAGCAGTACCTTG	331		
Db	739	GTACATCGGTACTACCGCGACTTCGTGCTCGAGCTCAACAAGGCGCTCG	788		

RESULT 15
US-09-902-540-8164
; Sequence 8164, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10

```

; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8164
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8164

```

Query Match	7.0%;	Score 41.6;	DB 3;	Length 969;
Best Local Similarity	43.9%;	Pred. No. 0.33;	225;	Indels 0; Gaps 0
Matches 176;	Conservative 0;	Mismatches 225;	Indels 0;	Gaps 0
Qy	21	CACCAGCACACAGAGACGCGGAAAGCGGGATGCGGCGCAAGAGCTGTTTGATGACCT	80	
Db	402	CACCAAGCTGAGCGAGACGCTGGACCCGGGACAGGTGCTGGAGTTGCTGGACGACTACTT	461	
Qy	81	GGGCGGCGCAGAGGCGATGAAGCTTGGCGGTTTGACACCTTTCAGATAGGTGCTGGCTGA	140	
Db	462	CGGGGCATATGGCCACATCTCATGCGCGCGCCACGGCATCGTGAAACAAGTTCTTGGGCGA	521	
Qy	141	CCCGGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATCAAGAGCAGAGAAGATGAAGCAGGT	200	
Db	522	CGGGATGCTCGGTGCTGGGGCGTTCCGGATCGCGCGAGNACCAACGCGGAGCTGGCCAT	581	
Qy	201	CAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAAGGGCCGGAAGCATGTACGA	260	
Db	582	CGCGGGCGCTCGACATGCGCGCCAAAGCTGGAGGACATCAAGCCAGCGCGTGACGCG	641	
Qy	261	CGCACAGCCCATCTGTTCAAGGGCCACGGCTTGGACCAACGGCCACTTTTGACAAGATCAA	320	
Db	642	AGGTCTTCCGCCGCTGGCGCATTCGGCATTCGGGCTGCACACCGGCATGTTGGCGGGCGGCAT	701	
Qy	321	GCAGTACCTTTGGAGAGACGCTGCAAGAGATGGGGCTCAAGCAGGATGTGATTCACGACGCG	380	
Db	702	GCTCGGGCGCGGAGCAGCAGCAGGTACACGTCATCGGTGACGCGGTGAACCTGGCGTC	761	
Qy	381	CGCCGGAGTGGTGGAGTCCACCCCGCAGCAATTTGACTTTC	421	
Db	762	TCGCGTGGAGGGCTTCAACCAAGTCTCCACGGCGGTGGACATCC	802	

Search completed: February 27, 2006, 21:58:07
Job time : 175 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	254.5	22.7	124	4	US-10-282-122A-61519	Sequence 6
2	148	12.2	324	4	US-10-425-114-58160	Sequence 5
3	142.5	13.7	19723	4	US-10-084-846A-5	Sequence 5
4	125	11.1	417	4	US-10-437-963-143835	Sequence 1
5	125	11.1	16995	4	US-10-084-846A-3	Sequence 6
6	124.5	11.1	19662	4	US-10-084-846A-6	Sequence 6
7	120.5	10.7	19608	4	US-10-084-846A-8	Sequence 8
8	119.5	10.7	276	4	US-10-437-963-166380	Sequence 1
9	117.5	10.5	384	4	US-10-425-114-72136	Sequence 7
10	117.5	10.5	384	4	US-10-425-114-72137	Sequence 7
11	117.5	10.5	19723	4	US-10-084-846A-5	Sequence 5

```
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61519
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Legionella pneumophila
US-10-282-122A-61519

Alignment Scores:
Pred. No.: 9,08e-16 Length: 124
Score: 254.50 Matches: 49
Percent Similarity: 64.1% Conservatives: 26
Best Local Similarity: 41.9% Mismatches: 41
Query Match: 22.7% Indels: 1
DB: 4 Gaps: 1

US-09-920-953-2 (1-598) x US-10-282-122A-61519 (1-124)
QY 61 AAGAAGCTGTTGATGACCTGGCGGCGGAGGAGGATGAAGCTGGCGGTTGACACCTTC 120
Db 3 GluSerLeuPheGluArgLeuGlyGlnAsnAlaValAsnThrAlaValAspPhe 22
QY 121 TAGCATAAGTGTGCTGACCCGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATGCAA 180
Db 23 TyrArgLysMetLeuMetAspAspValAsnTyrPhePheAspValAspMetGlu 42
QY 181 GACGAGAGATGACGAGGTCAAGTTCATGAGCTTCGTTGTCGGGAGCAGACCAATAC 240
Db 43 GlnGlnLeuLysGlnLysGlyPheLeuThrMetValPheGlyGlyProAsnGlnTyr 62
QY 241 AAGGCGGAGAGCTGATGACGACGACGACCCCATCTGGTCAAGGCGGACGCTGGACAC 300
Db 63 ThrGlyLysSerMetArgGluGlyHisGlnHisLeuLeu---AlaArgGlyLeuAsnAsp 81
QY 301 CGCCACTTTGACAAGATCAAGCAGTACTTGGAGAGACGCTGCAAGAGATGGCGTCAAG 360
Db 82 SerHisValAspLeuValIleGluHisLeuGlyGlnThrLeuLysGluLeuGlyAlaAsn 101
QY 361 CAGAGTGTATCCAGCAGCGCGCGGAGTGGTGGATGCCACCGCGAGAA 411
Db 102 GluGluAspIleGlnLysValAlaAlaIleAlaAsnSerValArgGlyAsp 118

RESULT 2
US-10-425-114-58160
; Sequence 58160, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 58160
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73219F07_FLI.pep
US-10-425-114-58160
```

```
Alignment Scores:
Pred. No.: 2,66e-05 Length: 324
Score: 148.00 Matches: 62
Percent Similarity: 38.1% Conservatives: 18
Best Local Similarity: 29.5% Mismatches: 77
Query Match: 13.2% Indels: 53
DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-10-425-114-58160 (1-324)
QY 5 TGCCTGCAGACGCGG-----CCACGACGACACGAGAGCGGCGGAGACGG 49
Db 84 CysAlaAlaArgThrArgAlaAlaArgThrThrAlaProSerAlaProCysThrArgArgThr 103
QY 50 GATGCGGCGCAGAGAGCTGTTTGATGACCTGGCGGCGCAGAGGATGATGAGCTGGCGG 109
Db 104 SerSerGlySerArgAlaCys-----CTGACCGGAGAGCTGCTGC 154
QY 110 TTGACACCTTCTACGATAAGGTGCTGG-----CTGACCGGAGAGCTGCTGC 154
Db 111 -----ProSerAlaAlaThrCysThrArgTTPAlaAlaThrArgSerArgProThrSer 128
QY 155 CTTCTCTGAGTCCCTGGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTCATGAGCT 214
Db 129 ProArgTTPGlyProTTPCysCysProSerProSer-----SerCysSerSerSerArgAla 147
QY 215 TCGTGTGTTGGCGGAGCAGACCAATACAGGCGGAGCATGTACGACGACACGCCCATC 274
Db 148 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProG1 167
QY 275 TGGT-----CAAGGCGCACGCGCTCGACACCGCCACTTTGACAAGATCAAGCAGTACC 328
Db 167 nGlyThrProArgProProArgPro--ThrSerArgThrSerSerAlaArgSerSerThr 186
QY 329 TTGGAGAGACGCTGCAAGAGA-----TGGCGCTCAAGCAGGAGTGTGATCC 373
Db 187 -----SerAlaCysThrArgProAlaAlaThrCysThrSerThrCysArgAlaThrTTP 204
QY 374 AGCAGCGCGCGGAGTGGTGGAGTCCACCGCGGACGAAATTTGACTTNCACCAACTGCG 433
Db 205 AlaCysAlaThrProThrTTPArgProProAlaProArgCysThrAlaSerAlaThr--- 223
QY 434 CACCCAACTGATTTTCAATTAACCAACCCAGCCTGAGCGCTCATTCCTCGATTTTGAG 493
Db 224 -----ProGlnAlaAlaSerGlyThrSerTTPArg 234
QY 494 -----CGGGAGCGCCAGTTGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCTGCA 565
Db 254 GlyArgAlaSerSerAlaThrAla 261

RESULT 3
US-10-084-846A-5
; Sequence 5, Application US/10084846A
; Publication No. US2004006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREPZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
```


; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 5

; LENGTH: 19723

; TYPE: PRT

; ORGANISM: Streptomyces viridochromogenes

; FEATURE:

; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.

; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.

US-10-084-846A-5

Alignment Scores:

Pred. No.:	0.000264	Length:	19723
Score:	142.50	Matches:	63
Percent Similarity:	35.0%	Conservative:	16
Best Local Similarity:	27.9%	Mismatches:	68
Query Match:	12.7%	Indels:	79
DB:	4	Gaps:	12

US-09-920-953-2 (1-598) x US-10-084-846A-5 (1-19723)

QY	5	TGCTGCAGACGGCCACACAGACAGCGGGAAGCGGATCGGGCGCAAGA	64
DB	4635	CysAlaAlaArgSerProSerPro-----AlaTrpSerThr	4647
QY	65	AGCTGTTTATGACCTGG-----GGGGCGCAGAGCATGAAGCTGGCGGTG	112
DB	4648	SerAlaProAlaThrTrpSerTrpThrSerAlaAlaThrAlaProCysTrpArgPro	4667
QY	113	ACACCTTCTACGATAAGGTGCTGGCTG-----	139
DB	4668	ThrProProThrGlyProAlaThrSerGluTrpThrProProProSerSerProArg	4687
QY	140	-----ACCCGG-----AGCTGCTGCCCTTCTCGAGTCCCTGGACATGCAAGACGAGAAGA	190
DB	4688	ProThrArgAlaAlaSerSerProThrSerSerHisThrCysSerAlaGlyAla	4707
QY	191	TCAGCAGTCAAGTTCATGAGTTCGTG-----TTGGCGGAGCGAGCC	235
DB	4708	AlaProArgSerSerProArgSerArgCysSerThrThrCysArgValProTrpSerSer	4727
QY	236	AATACAGGGCGGACGATGACGAG-----	262
DB	4728	CysGlyArgSerAlaAlaCysArgThrAlaSerGlyProSerArgAlaIleCysPro	4747
QY	263	-----CACACGCC-----AFTCGTCAAGGGCCACGGCTCGGACCAACCGCCACT	307
DB	4748	ArgCysSerThrProAlaProThrTrpSerAlaThrSerThrTrpThrThrGly	4767
QY	308	TTGACAGATCAAGAGTACCTTTGGAGACGCTGCAAGAGATGGCGCTCAAGCAGGATG	367
DB	4768	CysAlaArgSerSerGly-----TrpProSerAla-----	4777
QY	368	TGATCCAGACCGCCGGAGTGTGG-----AGTCACCGCGAGCAATTTGACTTNC	421
DB	4778	-----ProAlaArgTrpTrpMetProSerProSerProSerThr--AlaGluAlas	4793
QY	422	CCAACAACATGCGCACCACTGATTTTCATTAACCCAA-----	459
DB	4793	erArgSerCysTrpProAlaAlaAlaProLeuAlaArgSerThrSerArgArgTrpProA	4813
QY	460	-----CCCCAGCTGAGCGCTCATTCATCGATTTTGGAGCGGGAGCGCCAGTTCGCCAGGCC	517
DB	4813	laSerAlaProGluArgArg-----ThrCysProThrArgSerS	4826
QY	518	GCCCGGGGGCCCA	531
DB	4826	erProGlyGlyPro	4830

RESULT 4

US-10-437-963-143835

; Sequence 143835, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 143835
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44705C.1.pap
US-10-437-963-143835

Alignment Scores:			
Pred. No.:	0.0049	Length:	417
Score:	125.00	Matches:	63
Percent Similarity:	36.2%	Conservative:	13
Best Local Similarity:	30.0%	Mismatches:	74
Query Match:	11.1%	Indels:	60
DB:	4	Gaps:	10

US-09-920-953-2 (1-598) x US-10-437-963-143835 (1-417)

QY	23	CCAGCACCACAGAGACGGCGGAAGCGGATCGGGCGCAAGAAGCTGTTGTGACCTGG	82
DB	22	ProThrProHisArgArgGlu-----ileGluArgTrp	32
QY	83	GGGGCGCAGAGGATGAAGCTGGCGGTGACACCTTCTACGATAAGTGTGGTGGTACC	142
DB	33	Leu-----ProTrpArgSerAlaProPro-----ThrThr	43
QY	143	CGAGCTGTGTC-----CCTTCTCGAGTCCCTGGACATGCAAGAGCAGA	187
DB	44	GlySerCysSerThrProThrThrProProThrProProThrThrThrSer---	62
QY	188	AGATGAAGCAGCTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAAGGCC	247
DB	63	-----SerArgSerLeuProProAlaThrProProProAlaProThrIlysArg---	79
QY	248	GAAGCATGTACGACGACACACGCCCATCTGGTCAAGGGCCACGGCTGGACCAACCGCCACT	307
DB	80	-----ArgThrThrArgTrp-----GlyAlaThr	87
QY	308	TTGACAAGATCAAGCAGTACCTTGGAG-----AGACGCTGCAAG	346
DB	88	LeuThrAlaThrThrSerThrAlaGluAsnSerArgArgArgArgAlaArgArg	107
QY	347	AGATGGCGCTCAAGCAGATGTGATCCAGACCGCCGGAGTGGTGGAGTCCA-----	400
DB	108	ArgArgGlyArgSerArgAlaSerSerThrThrProProProThrThrSerProGlyThr	127
QY	401	---CCCCGCGAGAAATTTGACTTNNCCCAACAAGTGGCGACCCAACTGATTTTCATTAACCC	457
DB	128	SerProSerThrProSerAlaProSerThrSerSerProThrArgAlaSerProPro	147
QY	458	AACCCAGCTGAGCGCTCATTCATCGATTTTGGAGGGGGGCGCCAGTTCGCCGCGCG	517
DB	148	TyrArgSerThrSerSerSerProPro--ProAlaAlaSerSerAlaSerAlaAla	167
QY	518	GCCCGGGGGCCCA-----GGAGCTGCAATCGTTTG	550
DB	167	rgProProAlaProThrThrSerProThrArgProProSerGlyGlyCysAlaSerLeu	187
QY	551	CCAGCCCTTGTCTGTCATTGAAGGCCA	576


```
QY 233 TCCTGCTCCGCAACAGC----- 216
|||:|||||:|:|
Db 19429 SerSerProSerProArgProGlyCysThrGluGlyArgSerProValSer 19448
|||:|||||:|:|
QY 215 -----AAGCTCATGAACCTTGACCTGCTTCATCTCTGCTCTTGCATGTCACG 168
|||:|||||:|:|
Db 19449 SerProHisGlyArg-SerGlyCysTrpProAlaGlyProArgProAlaAlaGlyProG 19468
|||:|||||:|:|
QY 167 GACTCGAAGAGGCGAGCAGCTCCGGGTGAGCCAGCAGCAGCTTATCGTAGAAGGTGTCAACC 108
|||:|||||:|:|
Db 19468 YAspArgArgGlnAlaLeuSerSerGlySerPro----- 19479
|||:|||||:|:|
QY 107 GCAGCTTCATGCTTCTGCGCGCCAGGTGCATCAACAGCTTCTTGGCGCCGCGATCCC 48
|||:|||||:|:|
Db 19480 -----ArgArgArgGlyAlaProSerPheSerAlaAlaArgIleAl 19493
|||:|||||:|:|
QY 47 GCTTCG-----CGTCTCTGCTGGTGGTGG 20
|||:|||||:|:|
Db 19493 alaProThrIleProAlaLeuPheCysSerTrp 19504
|||:|||||:|:|
RESULT 7
US-10-084-846A-8
; Sequence 8, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREPFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 19608
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-8
Alignment Scores:
Pred. No.: 0.0363 Length: 19608
Score: 120.50 Matches: 49
Percent Similarity: 35.7% Conservative: 16
Best Local Similarity: 26.9% Mismatches: 92
Query Match: 10.7% Indels: 25
DB: 4 Gaps: 7
US-09-920-953-2 (1-598) x US-10-084-846A-8 (1-19608)
QY 20 CCACGACGACACAGAGCGGCGGAGCGGATCGGGCGCAAGAGCTGTTGTGAGCC 79
|||||:|:|:|:|:|
Db 5430 ProProAla-----SerSerThrArgCysCys----- 5438
|||||:|:|:|:|:|
QY 80 TGGCGCGCGCAGAGGCGATGAAGCTGGCGGTGACACCTTCTACGATAGGTGCTGGCTG 139
|||||:|:|:|:|:|
Db 5439 -----ProProAlaSerThrTrpArg-----SerThrAlaAlaCysTrpPro 5452
|||||:|:|:|:|:|
QY 140 ACCCGAGCTGCTGCCCTTCTTCGAGTCCCTGACATGCAAGAGCAGAGATGAAGCAGG 199
|||||:|:|:|:|:|
Db 5453 ArgArgProCysSerProArgThrArg-----ThrSerArgArgArgProGlyArg 5470
|||||:|:|:|:|:|
QY 200 TCAGTTTCATGAGCTTCGTGTTTG---GCGGAGCAGACCAATACAGGCCGGAAGCATGT 256
|||||:|:|:|:|:|
```

```
Db 5471 SerThrSerArgSerThrAlaThrProThrSerGlyCysSerProTrpCysProAlaCys 5490
QY 257 ACAGCGCACACGCCCTCTGGTCAAGGGCCACGCGCTGGACACCGCCACTTTGACAAGA 316
|||||:|:|:|:|:|
Db 5491 ThrSerAsnArgProAlaArgProProThrSerTrpProThrArgProArgSerAla 5510
|||||:|:|:|:|:|
QY 317 TCACGAGTACCTTGGAGAGAGCTGCAAGATGGCGTCAAGCAGGATGTATCCAGC 376
|||||:|:|:|:|:|
Db 5511 ProArgProSerThrSerArgSerThrAlaArgTrpProSerProAsnTrpSerArgAsp 5530
|||||:|:|:|:|:|
QY 377 ACGCCCGCGAGTGGTGGAGTCCACCGCGAGCAATTTGACTTNCACAACA-----ACT 430
|||||:|:|:|:|:|
Db 5531 TrpProThrSerThrProSerProAlaArgThrArgThrAlaProSerArgArgThr 5550
|||||:|:|:|:|:|
QY 431 GCGCACCCCACTGATTTTTCATTAACCAACCCAGCAGCTGAGCGCTCATTCATCGATTTT 490
|||||:|:|:|:|:|
Db 5551 ProArgProTrpProCysArgArgThrThrProSerAlaSerCysSerArg----- 5567
|||||:|:|:|:|:|
QY 491 GAGCGGGAGCGCCAGTTGCGAGCGCGCCAGGGGGCCAGGAGCTGCAATCGTTTG 550
|||||:|:|:|:|:|
Db 5568 ArgProArgThrProValTrpArgArgProGlyCysProProHisArgSerAlaArgLeu 5587
|||||:|:|:|:|:|
QY 551 CCAGCC 556
|||||:|:|:|:|
Db 5588 ProAla 5589
|||||:|:|:|:|
RESULT 8
US-10-437-963-166380
; Sequence 166380, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 166380
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(276)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_65095C.1.pep
US-10-437-963-166380
Alignment Scores:
Pred. No.: 0.0151 Length: 276
Score: 119.50 Matches: 52
Percent Similarity: 35.1% Conservative: 15
Best Local Similarity: 27.2% Mismatches: 69
Query Match: 10.7% Indels: 55
DB: 4 Gaps: 8
US-09-920-953-2 (1-598) x US-10-437-963-166380 (1-276)
QY 29 CCACAGACGCGCGGAGCGGATCGGGCGCGCAAGAGCTGTTGTGACCTGGCGCG 88
|||||:|:|:|:|:|
Db 3 ProArgArgArgArgArgArgIleCysThrValArg----- 14
|||||:|:|:|:|:|
QY 89 CAGAAAGCATGAAGCTGGCGGTGACAGCTTCTACGATAGGTGCTGGTGAACCGGAGC 148
|||||:|:|:|:|:|
```

```

Db 15 -----ArgProThrAlaThrThr-----ThrThrThrSer 25
QY 149 TGCTGCCCTTCTTCGAGTCCTCGACATGCAAGAGCAGAAGATGAAGCAGGTCAAGTTCA 208
Db 26 AlaSerProSerSerProThrPro-----GlySerSerProGly 39
QY 209 TGAGCTTCGTGTTGGCGGAGCAGACCAATPACAAAGGCGGAGCATGTATGACGCG-----262
Db 40 AlaAlaSerCysAlaThrSerSerAlaAlaSerArgAlaThrArgThrSerThrAlaPro 59
QY 263 ---CACAGCCCATCTGCTCAAGGCGCAGCGCTCGACCAACCCACTTTGACAAAGATCA 319
Db 60 ProSerSerProSerHisGlySerArgSerProTrpThrGlyThrThrSerSerProSer 79
QY 320 AGCAGTACCTTGGAGAGACGCTGC-----AAGAGATGGCGCTCAAGCAGGATGTGA 370
Db 80 ArgSerGlySerCysArgGlyCysCysPheArgArgArgTrpArgSerThrArg-----97
QY 371 TCAGCAGCGCGCGGAGTGTGTGAGTCCACCGCGCAGCAATTTGACTTNNCCCAACAAC 430
Db 98 -----ProProAlaProSerSerAlaSerProThrGly 108
QY 431 GCGCACCACCACTGATTTTCATTAAACCAACCCAGCGCTGAGCGCTCATTCATCGATTTT 490
Db 109 AlaSerThrThrSer-----ProSerProThr-----117
QY 491 GAGCGGGAGCGCGCAGTTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 550
Db 118 -----ProAlaAlaArgAlaAlaSerGlyAlaProAlaSerGlySer***Cys 133
QY 551 CCAGCCCTTGTGCTGATTTGAAGGCCATCAGCCCA 583
Db 134 SerGlyArgAlaProArgGluSerSerAlaPro 144

```

RESULT 9

```

US-10-425-114-72136
; Sequence 72136, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72136
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3245-558-A1_FLI.pep
US-10-425-114-72136

```

```

Alignment Scores: 0.0257 Length: 384
Pred. No.: 117.50 Matches: 69
Score: 37.9%
Best Local Similarity: 30.8% Mismatches: 74
Query Match: 10.5% Indels: 65
DB: 4 Gaps: 13

```

```

US-09-920-953-2 (1-598) x US-10-425-114-72136 (1-384)

```

```

QY 15 CGGGCCACAGCAGC-----CACAGAGCGCGGAGCGGATGCGGGCGCAAGAGCT 68
Db 54 ArgGlyHisArgHisSerSerHisArgProLeuAlaSerGlyArgGln-----69

```

```

QY 69 GTTTGATGACCTGGGCGCGCAGAGGCGATGAAGCTGGC-----107
Db 70 -----ArgArgArgArgGlyArgAlaGlyArgArgGlyGlyArgGlyGlu 84
QY 108 ---GGTTGACACCTTCTACGA-----TAAAGTGTCT 134
Db 85 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgArgAlaArgArgArgGlyAla 104
QY 135 GCGTCAACCGGAGCTGCTCCCTTCTTCAGTCCCTCGACATGCA-----AGAGCA 185
Db 105 ArgArgGlyGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGlyArgGlyAla 124
QY 186 GAAGTGAAGCAGGTCAAGTTCATGAGCTTCGTGTTGGGAGCAGACCAATACAGGG 245
Db 125 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 144
QY 246 -----CCGAGCATGTTACGACGCGCACACGCCCATCTGCTCAAGGGCCA 287
Db 145 LeuGluGlyGlyValArgProArgAlaAlaArgAlaAlaAlaGlySerArgGlyArg 164
QY 288 CGG-----CCTGGACCAACCGCCACTTTTGACAAAGTCAA 320
Db 165 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeu---GlnArgGly 183
QY 321 GCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGT-----CAAGCAGGATGT 368
Db 184 AlaGlyGlyValArgGluSer-----AspGlyArgAlaGlyValGlnAlaGlyAla 201
QY 369 GATCCAGCAGCGCGCGGAGTGTGGAGTCCACCGCGGAGCAAT---TTGACTTNCCTAA 425
Db 202 Asp--ArgProGluProGluAlaGluAlaArgProAlaAlaArgLeuLeuGlnGlyProA 221
QY 426 CAACTCGCGCACCAACTGATTTTCATTAAACCCCAACCCAGCCCTGAGCGCTCATTCATCG 485
Db 221 spAspLeuHisProAlaGlu-----ProLeuProSerMetProGlu-----234
QY 486 ATTTTGAGCGGGAGCGCCAGTTCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 545
Db 235 -----ProArgProGlyProArgArgGlyThrAlaGlnGlyArgArgProAspHisP 253
QY 546 GTTTGGCCA 553
Db 253 roValPro 255

```

RESULT 10

```

US-10-425-114-72137
; Sequence 72137, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72137
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3061-057-C6_FLI.pep
US-10-425-114-72137

```

```

Alignment Scores: 0.0257 Length: 384
Pred. No.: 117.50 Matches: 69
Score: 37.9%
Percent Similarity: 37.9%
Conservative: 16

```

```
Best Local Similarity: 30.8% Mismatches: 74
Query Match: 10.5% Indels: 65
DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-10-425-114-72137 (1-384)
QY 15 CCGCGCCACCCAGC-----CACAGACGCGGAGCGGATCGCGCGCGCAAGAGCT 68
DB 54 ArgGlyHisArgHisSerHisArgProLeuAlaSerGlyArgGln----- 69
QY 69 GTTTCATGACCTGGCGCGGCAAGGCGATGAAGTGGC----- 107
DB 70 -----ArgArgArgGlyArgAlaGlyArgGlyGlyArgGlyGlu 84
QY 108 ---GGTTGACACCTTCTACGA-----TAAGGTGCT 134
DB 85 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgArgAlaArgArgGlyAla 104
QY 135 GGCTGACCGGAGCTGCTCCCTTCTTGAGTCCCTGGACATGCA-----AGAGCA 185
DB 105 ArgAspGlyGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGluGlyArgAla 124
QY 186 GAAGATGAAGCAGGCTCAAGTTCATGAGCTTCTGTTGCGGAGCAGACCAATCAAGG 245
DB 125 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 144
QY 246 -----CCGAGCATGTATACAGCAGCACAGCGCCATCTGTCACAGGGCCA 287
DB 145 LeuGluGlyGlyValArgProArgAlaAlaAlaAlaAlaAlaGlySerArgGlyArg 164
QY 288 CGG-----CTGAGCACCCGCCACTTGTGACAGATGGCGT-----CAAGCAGATGT 368
DB 165 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeu---GlnArgGly 183
QY 321 GCAGTACCTTGAGAGACGCTCAAGAGATGGCGT-----CAAGCAGATGT 368
DB 184 AlaGlyGlyValArgGluSer-----AspGlyArgAlaGlyValGlnAlaGlyAla 201
QY 369 GATCCAGACGCGCGGAGTGGTGGAGTCCACCGCGCAGCAAT---TTGACTTCCCAA 425
DB 202 Asp--ArgProGluProGluAlaGluAlaArgProAlaAlaArgLeuGlnGlyProA 221
QY 426 CAACTGCGCACCACTATTTTCAATTAACCAACCCAGCGCTGAGCGCTCATTCATCG 485
DB 221 spAspLeuHisProAlaGlu-----ProLeuProSerWetProGlu----- 234
QY 486 ATTTGAGCGGAGGCGGAGTGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 545
DB 235 -----ProArgProGlyProArgArgGlyThrAlaGlnGlyArgArgProAspHisP 253
QY 546 GTTTCGCA 553
DB 253 rovalPro 255

RESULT 11
US-10-084-846A-5
; Sequence 5, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREPZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 5
; LENGTH: 19723
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-5

Alignment Scores:
Pred. No.: 0.0712 Length: 19723
Score: 117.50 Matches: 64
Percent Similarity: 32.9% Conservative: 13
Best Local Similarity: 27.4% Mismatches: 86
Query Match: 10.5% Indels: 71
DB: 4 Gaps: 15

US-09-920-953-2 (1-598) x US-10-084-846A-5 (1-19723)
QY 556 GGCTGGCAACGATTGTCAGGCTCTGGGCGCCCTGGGCGGCTCGGC----- 509
DB 16445 GlyAlaGlnArgArgCysHisArgThrGlyProIleGlyLysSerGlyAlaGlyProGly 16464
QY 508 -----AACTGGCGCTCCCGCTCAAAATCGATGGAATG 476
DB 16465 ThrAlaAlaArgGlnArgLeuValArgSerArgTrpProMetSerAlaSerAlaPhe 16484
QY 475 AGCGCTCAGGCTGGGGTTTAAATGAAATCAGTTGGTGGCGCAGTTGT----- 425
DB 16485 SerTrpLeuValGlyArgGly-----SerTrpAlaValSerCysAlaArgThr 16500
QY 424 -----TGG-----GNAAGTCAAAATCTGT 407
DB 16501 ProArgProGluProArgTrpArgArgSerProGlyGlyTrpArgThrSerProCysArg 16520
QY 406 CGCGGG-----TGACTCCACCACTCCGGCGCGCTGGGATCATCATCTCTGCTTCA 356
DB 16521 AlaGlySerSerSerTrpThrSerPro---ProArgArgProGlyAsnTrpProThrSer 16539
QY 355 CGCCCATCTCTTTCAGCGCTCTCCAAAGTACTGCTGTATCTGTCAAAGTGGCGGTGT 296
DB 16540 ThrProSer-----AlaArgThrArgTrpSerThrProSerAlaAlaThrGlyGlySer 16557
QY 295 CCAGCGCGTGGCGCTTGACACGATGGCGGTGTGCGT---CGTACATGCTTCGCGCCTTGT 239
DB 16558 ProAsnGlyThrTrpArgProThrAlaArgCysArgProAlaAlaCysTrpThrArgCys 16577
QY 238 ATTGCTGCTCGCGCAACAGAGCTCATGAACCTGACCTGCTTCATCTCTCTCTCTT 179
DB 16578 GlyGly-----ProArgAlaVal-----ProThrSerSerThrSerAla 16590
QY 178 GCATGT-----CCAGGGACTCGAAGAAGG--- 155
DB 16591 GlnCysTrpSerThrAlaArgProArgProValAsnArgProGlyProArgArgPro 16610
QY 154 GCAGCAGCTCCGGGTGACCCAGCACCTTATCTAGAGGTGTCAACCGCAGCTTCATCG 95
DB 16611 GlyArgArgProProThrAlaArgProAsnSerArgAlaArgPro-----Cys 16627
QY 94 CTTCTG-----CGCCGCCAGGTGCATCAACAGCTTCTTTCG----- 59
DB 16628 TrpArgProProArgArgAlaSerTrpArgAlaCysCysGlySerProThrTrpPro 16647
QY 58 GCCCGCATCCCGTCCCGCGCTCTCTGTGGTGTGGTGGCGCG 17
DB 16648 GlyArgAlaProArgArgSerAlaCysSerAlaGlyTrpPro 16661

RESULT 12
US-10-084-846A-7
; Sequence 7, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
```



```

|   ...   ...   ...   ...   ...   ...   ...   ...   ...   ...   ...   ...   ...   ...   ...   ...
123 o-----ArgArgAlaIleProTrpArgValArgThrProValHisAlaArgMe 141
336 -----GAGCGTGCA-----AGAGATGGCGTCAAGC 361
141 tAlaAlaGlyAlaAlaValProAlaThrGlyAspArgArgArgArgGlyArgAl 161
362 AGGATGTGATCCAGCAGCGCGCGAGTGTGGA-----GTCCACCGCGCAGCAATTG 415
161 aAlaAlaLeuProGluAlaHisArgSerGlyGlyArgAlaValProArg----- 178
416 ACTTNCCCAACACTGGCACCACCACTGATTTCATTAAACCAACCCAGCGCTGAGCGCT 475
178 ----- 178
476 CATTCCATCATTTTGGAGCGGAGCGCCAG-----TTGCCGAGCGC 517
179 -LeuProArgArgValGlnGlyArgHisAlaGlyHisAlaGlyValLeuProPro 198
518 GCCCAGGGGCCAGG 533
198 oArgArgAlaProArg 203

RESULT 15
US-10-425-114-63797
; Sequence 63797, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63797
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-OSFLM202018F10_FLI.pep
US-10-425-114-63797

Alignment Scores:
Pred. No.: 0.0435 Length: 517
Score: 115.50 Matches: 62
Percent Similarity: 35.6% Conservative: 16
Best Local Similarity: 28.3% Mismatches: 80
Query Match: 10.3% Indels: 61
DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-10-425-114-63797 (1-517)
QY 24 CAGCACACAGACAGCGCGA-----AGCGGGATG 53
; ArgHisGlyArgAspAlaGlyGlyuProArgHisProAlaAspArgThrAlaGlyArg 108
QY 54 CGGCGCGCAAGAAGCTGTTTCATCCCTGGCGCGCAGAGCGATCAAGCTGGCGGTGGA 113
109 HisAlaAspArgGlyGlnHisValProGlyArgArgAlaArgGluArgArgGlyGln 128
114 CACCTT-----CTACGATAAGTGTGGTGCACCGGAGCTGCTGCCCTTCTTCGA 164
129 HisCysHisAlaHisHisArgGluAspAlaAlaTrpProGlyAlaArgValLeu----- 146
165 GTCCCTGGACATGCA-----AGAGCA 185
147 GlyProGlyHisAlaGlyValProArgArgAspValAlaAlaValAlaArgArgVal 166

```

```
QY 186 GAAGATGACGAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAAAGG 245
Db 167 HisLeuArgLeuProAlaValHisGlnArgValProHisArgGlnProAspGln--- 185
QY 246 CCGAAGCATGTACGACGC-----ACAGGCCCATCTGGT--- 278
Db 186 LeuArgHisValAlaAlaAspProArgValGlyMetAlaProValAlaArgProArgGlyVal 205
QY 279 -----CAAGGCCACGGCCTGGACCAACCGCCACTTTTGACAAGATCAAGCAGTA 326
Db 206 ProGlyArgArgHisGlyArgGlyValHisProGlyHisAlaGlnProGly 225
QY 327 CCTTGGAGACGCT-----GCAAGAGATGGCGT 356
Db 226 ProAlaArgGluAlaArgProArgProArgArgAlaProAlaGlyAlaArgGlnGlyArg 245
QY 357 CAAGCAGGATGTGATCCAGCACGCCCGGAGTGGTGGAGTCCACCCGCGCAATTTGA 416
Db 246 Arg-----ArgArgArgValGlnArgHisProArgArgArgGly 259
QY 417 CTNCCCAACAACCTGGCCACCCAACTGATTTTCATTAAACCAACCCCGAGCTGAGCGCTC 476
Db 260 AlaArgProGlnGluArgGlyArgValProAlaAspProAla-----AlaArg 276
QY 477 ATTCCATCGATTTTGAGCGGGAGCGCCAGTTGCCGAGCGCGCCAGGGGGCCCGAGG 533
Db 277 ValProAlaValProGlyHisGlyHisArgValProGlyValProGlnProHisArg 295
```

Search completed: February 27, 2006, 09:18:53
Job time : 157.5 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 27, 2006, 09:14:54 ; Search time 1.7 Seconds
(without alignments)
1047.362 Million cell updates/sec

Title: US-09-920-953-2
Perfect score: 1122
Sequence: 1 ggcgtcgtcgagacgcggc.....agccatttcgaccacgcc 598

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 117670 seqs, 14887254 residues
Total number of hits satisfying chosen parameters: 235340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-O=/abs/ABSSWEB spool/US09920953/runat_27022006_065351_20551/app query fasta_1
-DB=Published Applications AA_New -QPM=fastan -SUFFIX=rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MAIRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abs02np
-USER=US09920953 @CGN 1.1.7 @runat_27022006_065351_20551 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -FGAPOP=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0 -DELOP=6 -DELEXT=7

Database : Published Applications AA_New.*

Result No.	Score	Query Match	Length	ID	Description
C 1	104	9.3	1733	7 US-11-182-016-21	Sequence 21, Appl
C 2	101.5	9.0	279	7 US-11-072-512-3382	Sequence 3382, Ap
C 3	99.5	8.9	1742	7 US-11-182-016-23	Sequence 23, Appl
C 4	98.5	8.8	495	7 US-11-182-016-31	Sequence 31, Appl
C 5	93.5	8.3	1730	7 US-11-182-016-19	Sequence 19, Appl
C 6	89.5	8.0	205	6 US-10-689-742-72	Sequence 72, Appl
C 7	89.5	8.0	226	7 US-11-148-012-2	Sequence 2, Appl
C 8	89.5	8.0	891	7 US-11-182-016-38	Sequence 38, Appl
C 9	88	7.8	495	7 US-11-182-016-31	Sequence 31, Appl

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C 10	87.5	7.8	173	7 US-11-087-227-22	Sequence 22, Appl
C 11	87.5	7.8	173	7 US-11-087-227-79	Sequence 79, Appl
C 12	87.5	7.8	7968	7 US-11-186-731-5	Sequence 5, Appl
C 13	86.5	7.7	354	7 US-11-072-512-3151	Sequence 3151, Ap
C 14	86.5	7.7	553	6 US-10-453-372-1164	Sequence 1164, Ap
C 15	86.5	7.7	591	6 US-10-770-726-71	Sequence 71, Appl
C 16	86	7.7	252	7 US-11-072-512-2305	Sequence 2305, Ap
C 17	85.5	7.6	318	6 US-10-821-234-1117	Sequence 1117, Ap
C 18	85	7.6	460	7 US-11-182-016-26	Sequence 26, Appl
C 19	85	7.6	495	7 US-11-219-995-2	Sequence 2, Appl
C 20	85	7.6	602	7 US-11-072-512-3324	Sequence 3324, Ap
C 21	84.5	7.5	138	6 US-10-667-295-176	Sequence 176, App
C 22	84.5	7.5	181	7 US-11-175-690-344	Sequence 344, App
C 23	84.5	7.5	181	7 US-11-175-690-345	Sequence 345, App
C 24	84.5	7.5	181	7 US-11-175-690-346	Sequence 346, App
C 25	84.5	7.5	181	7 US-11-175-690-347	Sequence 347, App
C 26	84.5	7.5	181	7 US-11-175-690-348	Sequence 348, App
C 27	84.5	7.5	181	7 US-11-175-690-349	Sequence 349, App
C 28	84.5	7.5	218	6 US-10-667-295-151	Sequence 151, App
C 29	84.5	7.5	790	7 US-11-175-690-257	Sequence 257, App
C 30	84.5	7.5	790	7 US-11-175-690-258	Sequence 258, App
C 31	84.5	7.5	790	7 US-11-175-690-259	Sequence 259, App
C 32	84.5	7.5	790	7 US-11-175-690-260	Sequence 260, App
C 33	84.5	7.5	790	7 US-11-175-690-261	Sequence 261, App
C 34	84.5	7.5	790	7 US-11-175-690-262	Sequence 262, App
C 35	84.5	7.5	1717	7 US-11-182-016-20	Sequence 20, Appl
C 36	84.5	7.5	1744	7 US-11-182-016-22	Sequence 22, Appl
C 37	84	7.5	354	7 US-11-072-512-3151	Sequence 3151, Ap
C 38	83.5	7.4	1057	7 US-11-149-003-6	Sequence 6, Appl
C 39	82.5	7.4	226	7 US-11-148-012-3	Sequence 3, Appl
C 40	82.5	7.4	400	7 US-11-183-205-46	Sequence 46, Appl
C 41	82.5	7.4	678	7 US-11-072-512-3295	Sequence 3295, Ap
C 42	82	7.3	241	6 US-10-467-657-5632	Sequence 5632, Ap
C 43	82	7.3	419	7 US-11-171-531-2	Sequence 2, Appl
C 44	82	7.3	578	7 US-11-037-243-100	Sequence 100, App
C 45	82	7.3	627	7 US-11-037-829A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-11-182-016-21
; Sequence 21, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US/09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1733
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Grub
US-11-182-016-21

Alignment Scores:	
Pred. No.:	0.042
Score:	104.00
Percent Similarity:	30.9%
Best Local Similarity:	25.4%
Query Match:	9.3%
DB:	7
Length:	1733
Matches:	69
Conservative:	15
Mismatches:	76
Indels:	113
Gaps:	14

US-09-920-953-2 (1-598) x US-11-182-016-21 (1-1733)

QY 541 TGCAGGCTCTG-----GGCCCCCTGGCGCGCTCGGCAACTGGCGCTCC 497

Db	656	CysProLeuLeuLeuGluProAlaGlnGlyProLeuPro			-----HisSer	670
Qy	496	CCGCTCAAAATCGATGAATGAGCGCTGAGCTGGGTTGGTTAATGAAATCAGTTGG			-----	437
Db	671	ProLeuHisMetGly			-----	685
Qy	436	GTGGCAGTTGTTGGGNAAGTCAAATTCGTCGGGGTGG			-----	398
Db	686	AlaGlnGlyCysTrpGlyAla			-----AlaArgSerGlyTrpAlaArgGlyCysGlyAlaPro	704
Qy	397	-----			-----ACT	395
Db	705	ThrGlyProLeuHisCysTrpHisArgLeuProAlaValValGlySerProValGlySer			-----	724
Qy	394	CCACCACTCGGGCGGTGTCGATCAT			-----CTGCTTGA	356
Db	725	ProProLeuProGlyValAlaGlySerSerLeuAlaLeuGlySerGlyProGlySer			-----	744
Qy	355	CGCCCATCTCTGCGAGGTCTCTCCAAGGTACTGCTTGTCAAGTGGCGGTGGT			-----Gly	296
Db	745	GlyProLeuLeuAlaGlyLeuLeu			-----GlyCysPro	756
Qy	295	CCAGCGCGTCCCTGACAGATGGCGTGTGCTGATCATCTTCGCGCCCTTGATT			-----	236
Db	757	ProGlyProGlyProAlaSerProGlyArgCysArgHisTrpAlaLeuGlyProAlaAla			-----	776
Qy	235	GGT			-----CTGCTCCGCCAACACGAGC	212
Db	777	GlyProValGlnProAlaGlnProProAspProAlaGlnLeuLeuProAlaGlnSer			-----	796
Qy	211	TCATGAAT			-----TGACCTGCTTCATCTCTCTCTGCA	176
Db	797	ProHisProProLeHisValProAlaGlyArgSerAlaValAlaAlaGlyProAspGly			-----	816
Qy	175	-----			-----TGCTCAGGACTCGAAGAGGCGCAGCT	146
Db	817	GlyHisSerGlnProAlaProAlaValGlnArgTrpProAlaProSerGlyArgTrp			-----	836
Qy	145	-----			-----CCGGTCAGCCAGCACCTTATCGT	122
Db	837	HisSerProGluProGlyProProValProGlyProGlyAlaProGlyProGlnArg			-----	856
Qy	121	AGA			-----AGGTGTCA-ACGCCAGCTTC	99
Db	857	LyHisGlyLeAlaAlaLeuSerProAlaGlyGlnThrArgCysProGlnAlaGlnSer			-----	876
Qy	98	ATGCTCTCTGCGCGCCAGGTCTCAACAGCTTCTTGGCCCG			-----CATCCCGCTTCC	42
Db	877	LeuProAlaAlaProProLeuGlyProArgAlaThrAlaThrProAlaGlyValAlaAla			-----	896
Qy	41	GCCGTCTCTGTGTGGTGGCGCGCTCTGCAGC			-----	6
Db	897	GlyThrAlaAlaAlaLeuAlaAlaAlaArgAlaGly			-----	908

RESULT 2

US-11-072-512-3382

Sequence 3382, Application US/11072512

Publication No. US2006002945A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO

APPLICANT: SUGIYAMA, TOMOYASU

APPLICANT: OTSUKI, TETSUJI

APPLICANT: OTSUKI, TETSUJI

APPLICANT: WAKAMATSU, AI

APPLICANT: SATO, HIROYUKI

APPLICANT: ISHII, SHIZUKO

APPLICANT: YAMAMOTO, JUN-ICHI

APPLICANT: ISONO, YUUKO

APPLICANT: HIO, YURI

APPLICANT: OTSUKA, KAORU

APPLICANT: NAGAI, KEIICHI

APPLICANT: IRIE, RYOTARO

APPLICANT: TAMECHIKA, ICHIRO

APPLICANT:	SEKI, NAOHIKO		
APPLICANT:	YOSHIKAWA, TSUTOMU		
APPLICANT:	OTSUKA, MOTOKYUKI		
APPLICANT:	NAGAHARI, KENJI		
APPLICANT:	MASUHO, YASUHIKO		
TITLE OF INVENTION:	Novel full length cDNA		
FILE REFERENCE:	084335-0191		
CURRENT APPLICATION NUMBER:	US/11/072,512		
CURRENT FILING DATE:	2005-03-07		
PRIOR APPLICATION NUMBER:	US 60/350,978		
PRIOR FILING DATE:	2002-01-25		
PRIOR APPLICATION NUMBER:	JP 2001-379298		
PRIOR FILING DATE:	2001-11-05		
NUMBER OF SEQ ID NOS:	4096		
SOFTWARE:	PatentIn Ver. 2.1		
SEQ ID NO 3382			
LENGTH:	279		
TYPE:	PRT		
ORGANISM:	Homo sapiens		
US-11-072-512-3382			
Alignment Scores:			
Pred. No.:	0.0606		
Score:	101.50		
Percent Similarity:	31.6%		
Best Local Similarity:	26.7%		
Query Match:	9.0%		
DB:	7		
US-09-920-953-2 (1-598) x US-11-072-512-3382 (1-279)			
QY	528	GCCTCTGGCGGCTCGCAAC-----TGGCGCTCCCGCTC	491
DB	37	SerProTrpAlaSerSerTrpArgAlaAlaLeuTrpSerTrpArgProProArg	56
QY	490	AAATCGATCGAATGAGCGCTCAGCTGGGTGGTTAATGAAATCAGTTGGTGGCGC	431
DB	57	SerSerProSerLeuLeuArgGlyProGlyArg-----AlaPro	71
QY	430	AGTTGTTGGNAAGTCAAAATTCGTCCGGGTGGAATCCACCCTCCGGCGGCTGGGA	371
DB	72	ThrCysTrpProLeuArgValArgMetProTrp-----ArgAlaGly	85
QY	370	TCACATCTCTGAGCGCCATCTCTTGACGCGCTCTCTCAAGGTACTGCTGATCTTGT	311
DB	86	SerArgProCysArgValProAlaSerThr-----ThrCys	97
QY	310	CAAGTGG-----CGGTGTCAGGCGCGTGGCCCTTG-----ACCAGATGGCGGTGTG	263
DB	98	--GlyTrpTrpCysAlaSerTrpSerSerTrpArgLeuTrpValAlaTrpProCysP	117
QY	262	CGTCTGATCTGCTCCGCCCTTGT-----	239
DB	117	roSer--ProSerProSerProCysProCysProArgProCysProLeuProTrpProGln	136
QY	238	-----ATTGCTGCTGCCCAACACGAAGCTCATGAACCTTGACCTGCTTCTCTCT	185
DB	137	SerHisProCysLeuLeuProGlnProArgSerGln-----	148
QY	184	GCTCTTGTGATGTCAGGAGCTCGAAGAGGCGCAGCTCCGGGTGACGACCTTAT	125
DB	149	-----ProCysPro-----CysProAlaGlyProValProSer	159
QY	124	CGTAGAAGGTGTCACCGCCAGCTTATGCTTCTGCGCGCCCGCAGGT-----	77
DB	160	ArgProArgArgMetAlaAlaLeuSerGlyAlaLeuArgProProSerGlyLeuAspPro	179
QY	76	-----CATCAACAGCTTCTTGGCGCGCATCCGCTTCCCGCTCTCTCTGG	29
DB	180	SerProLeuHisHisArgLeuAlaAlaGlyProArgHisProThrGlyPro-----Trp	197
QY	28	TGCTGTGGCGCG	17

Db 198 ThrTrpProPro 201

RESULT 3

US-11-182-016-23

; Sequence 23, Application US/11182016

; Publication No. US20060019294A1

; GENERAL INFORMATION:

; APPLICANT: SUGEN, INC.

; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS

; FILE REFERENCE: 038602/0102

; CURRENT APPLICATION NUMBER: US/11/182,016

; CURRENT FILING DATE: 2005-07-15

; PRIOR APPLICATION NUMBER: US/09/958,359

; PRIOR FILING DATE: 2002-02-05

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 1742

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: Grub

US-11-182-016-23

Alignment Scores:

Pred. No.:	0.108	Length:	1742
Score:	99.50	Matches:	66
Percent Similarity:	37.0%	Conservative:	8
Best Local Similarity:	33.0%	Mismatches:	45
Query Match:	8.9%	Indels:	81
DB:	7	Gaps:	15

US-09-920-953-2 (1-598) x US-11-182-016-23 (1-1742)

QY 526 CCCTGGCGCGCTGGCACTGGCGCTCCCGCTCAAAATCGATGATGAGCGCTAG 467

Db 681 ProHisGlyAlaArgGluGlnTrp-----AspGly-----AlaGly 692

QY 466 GCTGGGGTTGGGTTAATGAAATCACTGGGTGCGCAGTTGTTGGGNAAGTCAAAATCGT 407

Db 693 ArgGlyProGlyLeuLeuGlySer-----LysGluLeuArg 705

QY 406 CGCGGG-----TGGACTCCACCCTC-----CGG 383

Db 706 LeuGlyGluGlyLeuArgGlyProHisTrpAlaProProLeuLeuAlaProSerAlaArg 725

QY 382 CGCGGTGCTGGATCATCTGCTGACGCCA---TCTCTGACGCTCTCTCCAGGT 326

Db 726 ArgArg-----ArgProArgGlyLeuAlaSer--SerProArgC 738

QY 325 ACTGCTTGATCTTGTCAAAGTGGCGGTGTTCAGGCGCGTGGCTTGACAGATGGCGT 266

Db 738 yscysrtpileuLeuSerSerSerTrpGlnArgAlaTrpGlnArg-ProHisSerArg 757

QY 265 GTGCGGTGTACATGCTTCGCGCTTGTATGTGCTCTCCG-----CAACACGA 215

Db 758 -----ArgAlaAlaGlyLeuProArgSerArgAlaArgAlaArg 770

QY 214 AGCTCATGAACTGACTGCTGCTCATCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 155

Db 771 IleSerTrpLysValProAlaLeuGlySer-----GlyAlaArgArgArg 785

QY 154 GCAGCAGCT-----CGGGTTCAGCCAGCCTTATCGTAGAGGTGT 113

Db 786 AlaSerAlaAlaSerThrAlaSerArgProGly---ProAlaProAlaSerArg---802

QY 112 CAACGCCAGCTTCATGCTCTTCTGCGCGCCAGGTCATCAACAGCTTCTTGGCGCCGC 53

Db 803 AlaLysProSerSer-----ThrHisSerCysAla---812

QY 52 ATCCCGCTTCCGCGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1

Db 813 -----CysTrpLysLysArg-CysSerArgArg 821

RESULT 4

US-11-182-016-31

; Sequence 31, Application US/11182016

; Publication No. US20060019294A1

; GENERAL INFORMATION:

; APPLICANT: SUGEN, INC.

; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS

; FILE REFERENCE: 038602/0102

; CURRENT APPLICATION NUMBER: US/11/182,016

; CURRENT FILING DATE: 2005-07-15

; PRIOR APPLICATION NUMBER: US/09/958,359

; PRIOR FILING DATE: 2002-02-05

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 31

; LENGTH: 495

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: Tks 118

US-11-182-016-31

Alignment Scores:

Pred. No.:	0.12	Length:	495
Score:	98.50	Matches:	64
Percent Similarity:	31.9%	Conservative:	18
Best Local Similarity:	24.9%	Mismatches:	62
Query Match:	8.8%	Indels:	113
DB:	7	Gaps:	15

US-09-920-953-2 (1-598) x US-11-182-016-31 (1-495)

QY 531 TGGGCCCCCTGGCGCGCTCGGCAACTGGCGCTCCCGCTCAAAATCGATGATGAGCG 472

Db 179 TrpAlaPro-----AlaProGlnGlnGlyAspLeuProTrpAla 191

QY 471 CTCAGCTGGGTTGGGTTAATGAAATCAGTTGGTGGCGAGTTGTTGGGNAAGTCAAA 412

Db 192 LeuArg-TrpGlnGlnLeuAlaLeuCysGlnSerGlySer--LeuValGlyAlaAla 210

QY 411 TTCGTGGGGTGGGACTCCACCCTCCGCGCGGTGCTGGATCAGATCCTCTTGGCGCC 352

Db 210 rAlaGlyArgGlySerSerAlaCysGlnAlaGluAspTrp-----223

QY 351 CATCTTTGCAGCGTCTCTCAAGGTACTGCTGTGATCTTGTCAAGTGGCGGTGGTCCAG 292

Db 224 -----ArgTrpArgTrp---Tr 228

QY 291 GCCGTGGCCCTTG-----ACCAGATGGCGGTGTCGTCGTA 256

Db 228 pThrTrpProSerProSerAlaLysSerProSerGlyAlaArgGlnThrProAlaHisph 248

QY 255 C---ATGCTTGGCCCTTGTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 205

Db 248 eGlySerLeuLysProLeuLeuAlaAlaAlaProThrSerCys-SerGlyGlyTrpProA 268

QY 204 CTGTGACCTGCTTCATCTCTGCTCTTGCATGCTCCAGGACTCGAAGAGGCGAGCA---G 148

Db 268 rgHisProAlaProAspSer-----AlaAlaProGlyValGlnProHisAlaAlaHisA 286

QY 147 CTCGCGGTGAGCAGCAGCAGCCTTAT-----CGTAGAAGGTGTCACCGCCAG 103

Db 286 laProGlyAlaProAlaProAlaAlaAlaValProProArgProAlaAlaPheProProA 306

QY 102 CT-----TCATGCTTCTGCGC-----86

Db 306 laAspGlySerProProProSerLeuLeuTrpProArgSerCysLeuTrpGlnProPheS 326

QY 85 -----CGCC 82

Db 326 erGlnThrArgHisTrpSerSerGlyThrGlnSerProLeuGlyProGlyValProArgP 346

```
QY 81 CAGGTGTCAT-----CAACACAG 67
Db 346 roGlySerGlyHisSerProCysGluSerCysSerTrpHisLeuLysProTrpProS 366
QY 66 CTTCTTGGCGCGCATCCCGTTCCGCGC-----38
Db 366 erProCysThrGlnAlaProHisProProArgProValArgTrpSerHisGlyProProS 386
QY 37 --TCTCTGTGTGCTGG-----TGGCGCGCTCTGCAGGCAGCG 2
Db 386 erGlySerTrpProTrpCysArgGlyTrpHisArgLeuProSerAla 401

RESULT 5
US-11-182-016-19
; Sequence 19, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; CURRENT FILING DATE: 2005-07-15
; PRIOR FILING DATE: 2005-09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 1730
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Grub
US-11-182-016-19

Alignment Scores:
Pred. No.: 0.381 Length: 1730
Score: 93.50 Matches: 50
Percent Similarity: 38.9% Conservative: 32
Best Local Similarity: 23.7% Mismatches: 86
Query Match: 8.3% Indels: 43
DB: 7 Gaps: 10

US-09-920-953-2 (1-598) x US-11-182-016-19 (1-1730)
QY 583 TGGCTGATGCTCTTAATGACGAGCGGTGGCAACAGATTGTCAGGCTCTGGGCCCC 524
Db 1230 TrpArgLeuAlaLeuThrCysPro-----GluProCysSerSerLeuTrpAsnSer 1246
QY 523 CTGGCGCGCTCGGCAACTGGCGCTCCCGCTCAAAATCGATGGAATGAGCGCTCAGGCT 464
Db 1247 LeuGlyMetGlyGlySerTrpArgSerSerGlyLysLeu---GlyLeuSerSerValLeu 1265
QY 463 GGGGTTGGGTTAATGAAATCAGTTGG-----GTGCGC 431
Db 1266 SerAlaGlyProLeuGlyLeuLeuTyrSerCysSerGlyAsnLysArgProValAlaGlu 1285
QY 430 AGTTGTTGG-----GNAAGTCAATTCGTCCGCGGTGAGCTCCACCA 389
Db 1286 ThrCysTrpProTrpArgCysValAlaValArgSerArgSerArgAspSerSerCys 1305
QY 388 CTCGGCGCGGTGCTGGATCACATCCCTGCTGAGCGCCCATCTCTTGAGCGTCTCTCAA 329
Db 1306 IleGluThrProSerLeuSerValAlaGluArgSerAlaPheAlaMetSerPheSer 1325
QY 328 GGTACTGCTTGTATCTTCAAGTGGCGGTGGTCCAGCGCGTCCCTTGCACCATGAGG 269
Db 1326 SerSerIleSerSerCysSerAlaSerSerArgAlaLeuLysGly-----1341
QY 268 CGTGTGGCTGATCATGCTTC-----GGCCCTGTGATTGCTGTGCTCCGCCAACACGA 215
Db 1342 -----GlnArgCysLeuPheThrSerArgProLeuArgLeuIleTrpGlyGlnLys 1359
QY 214 AGCTCATGAATTTGACCTGCTTCATCTCTGCTCTTGCATGCT-----CCAGGGGACT 164

RESULT 6
US-10-689-742-72
; Sequence 72, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-72

Alignment Scores:
Pred. No.: 0.735 Length: 205
Score: 89.50 Matches: 42
Percent Similarity: 29.6% Conservative: 19
Best Local Similarity: 20.4% Mismatches: 70
Query Match: 8.0% Indels: 75
DB: 6 Gaps: 7

US-09-920-953-2 (1-598) x US-10-689-742-72 (1-205)
QY 520 GGGCGCTCGGCAACTGGCGCTCCCGCTCAAAATCGATGGAATGAGCGCTCAGGCTGGG 461
Db 4 GlyGlyLeuGlyAlaTrpSerAlaGlySerSerValSerAlaPheHisSerThrAsnAla 23
QY 460 GTTGGGTTAATGAAATCAGTTGGTGGCGGCTGGTGGGNAAGTCAAAATTCGTCGGGG 401
Db 24 ValSerValPheSerLeuLeuPheArgAlaCysThrProValProAspProAlaPro 43
QY 400 TGGACTCCACCACTCCGCGCGGTGCTGGATCACATCTCTGCTTGAAGCCCATCTCTTGCA 341
Db 44 TrpProIleProCysArgGlyAlaSerGly-----53
QY 340 GCGTCTCTCCAGGTACTGCTTGATCTTGTCAAAGTGGCGGTGGTCCAGCGCGTGGCCCT 281
Db 54 -----LysLysThrGlyArgProAlaArg-----61
QY 280 TGACACAGATGGCGGTGGGTGCT-----257
Db 62 -----AlaArgLeuArgGlyHisProAlaSerProProThrAlaArgCysLeu 78
QY 256 ACATGCTTCGGCCCTTGTATTGCTGCTCCGCGCAACACGAAGCTCATGAATGACCT 197
```

Db 79 ThrCysPhe-----AlaThrAspSerCysSerGlnPro 89
QY 196 GTTCAATCTTCGCTCTTCATGTCACAGGACTCGAAGAGGCGACGCTCGGGTCTAG 137
Db 90 LeuGlyAlaSerValPheGlyValGlyGluLeuLeuArgAspCysAla-----Arg 106
QY 136 CCAGCACCTTATCGTAGAGGTCTCAA-----CGGCCAGCT 101
Db 107 ProArgProProThrLeuLeuGlyCysGlnHisGlnHisGlnPheArgHisThr 126
QY 100 TCATGCTCTTCGCGCGCCGAGCTCATCAACAGCTCTTCGCGCCGCGATC-----50
Db 127 AlaLeuArgThrArgArgProGlyArgPheValSerSerCysIleLeuSerProCys 146
QY 49 -----CCGCTTCGCGCTCT 35
Db 147 ProLeuLeuProLeuProValPheLeuLeuPhePheSerProPheProSer 166
QY 34 CTGTGCTGTGTGGCGG 17
Db 167 LeuSerAlaPhePhePro 172

RESULT 7

US-11-148-012-2
; Sequence 2, Application US/11148012
; Publication No. US20060008798A1
; GENERAL INFORMATION:
; APPLICANT: Chien, David Ying
; APPLICANT: Rang, Yiu-Lian
; APPLICANT: Tabrizi, Arita
; TITLE OF INVENTION: RABBIT MONOCLONAL ANTIBODIES TO HEPATITIS B SURFACE ANTIGENS AND
; FILE REFERENCE: METHODS OF USING THE SAME
; CURRENT APPLICATION NUMBER: US/11/148,012
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: 60/577,561
; PRIOR FILING DATE: 2004-06-07
; PRIOR APPLICATION NUMBER: 60/583,734
; PRIOR FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: amino acid sequence for the sag wild-type adw antigen
US-11-148-012-2

Alignment Scores:
Pred. No.: 0.741 Length: 226
Score: 89.50 Matches: 43
Percent Similarity: 31.2% Conservative: 17
Best Local Similarity: 22.4% Mismatches: 54
Query Match: 8.0% Indels: 78
DB: 7 Gaps: 11

US-09-920-953-2 (1-598) x US-11-148-012-2 (1-226)

QY 512 CGCAACTCGCGCTCCCGCTCAAAATCGATGAATGAGCGCTCAGGCTGGGGTGGGT 453
Db 24 ArgIleLeuThrIlePro-----GlnSerLeuAspSerTrp---TrpThr 37
QY 452 AATGAAATCAGTTGGTGGCGAG-----TTGTTGGNAAGTCAAAATCGTCGCGGGTG 399
Db 38 SerLeuAsnPhelGlyGlySerProValCysLeuGlyGlnAsnSerGlnSerProThr 57
QY 398 GACTCCACCACTCCGCGCGGCTCGTGGATCACATCTGCTTCAGCCCATCTCTTCAGC 339
Db 58 SerAsnHisSerProThrSerCys-----65
QY 338 GTCTCTCAAGGACTGCTGTGATCTTTCAAGTGGCGGTGGTCCAGGCGGTGGCCCTTG 279

Db 66 -----ProProlleCys-----ProGly 71
QY 278 ACCAGATGGCGTGGCTGCTGACATGCTTCGGCCCTTGATTTGGTCTGCTCCGCCAAAC 219
Db 72 TyrArgTrpMetCysLeuArgArgPheIleIlePheLeuPhe-----85
QY 218 ACGAGACTCATGAACCTGACCTGCTTCATCTTC-----186
Db 86 -----IleLeuLeuLeuCysLeuIleLeuLeuValLeuLeuAspTyrGlnGly 102
QY 185 -----TGCTCTTCATGCTCCAGGACTCGAAGAGGCGAGCAGCTCCCGGTCA 138
Db 103 MetLeuProValCysProLeuIle-----ProGlyThrThrThrThrSerThrGlyPro-----120
QY 137 GCCAGACCTTATCGTAGAAGGTGTCAACCGCCAGCT-----TC 99
Db 121 -----CysLysThrCysThrThrProAlaGlnGlyAsnSerMetPheProse 136
QY 98 ATGCCTTCTGCGCGCCGAGGTCTCAACAGCTCTTCGCGCCGCGCTCCGCTCCGCC 39
Db 136 rCysCysThrLysProSerAspGlyAsnCysThrCys-----IleProlleProse 154
QY 38 GTCT-----CTGTGTGTCTGG 23
Db 154 rSerTrpAlaPheAlaLysTyrLeuTrpGluTrp 165

RESULT 8

US-11-182-016-38
; Sequence 38, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US/09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 891
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Tks 202
US-11-182-016-38

Alignment Scores:
Pred. No.: 0.835 Length: 891
Score: 89.50 Matches: 58
Percent Similarity: 34.1% Conservative: 13
Best Local Similarity: 27.9% Mismatches: 68
Query Match: 8.0% Indels: 69
DB: 7 Gaps: 12

US-09-920-953-2 (1-598) x US-11-182-016-38 (1-891)

QY 535 CTCCTGGGCGCCCTCGGCGCTCGCG-----AACTGG 503
Db 643 IleLeuAlaProGlnGlyCysPheGlyThrArgTyrLeuAlaLeuLeuTrpGluThrTrp 662
QY 502 CGCTCCCGCTCAAAATCGATGAATGAGCGCTCAGGCTGGGGTGGGTTAATGAAATC 443
Db 663 LeuArgProGlnValAlaProGlyAsnProAlaLysProGly-----ArgAsp 678
QY 442 AGTTGGGTGCGCAGTTGTTGGNAAGT-----416
Db 679 SerProGlyArgThrArgTrpProAlaProProArgProArgLeuArgProPro 698
QY 415 CAAATTCGTGCGGGTGGAGTCCACACTCCCGCGCGTGTGGATCATCATCTGCTTGA 356

```

Db      699 ArgCysArgValSerProAlaProGlnThrArgArgAlaArgAspProGluAspPro 718
QY      355 CGCCATCTCTTGCAGCGTCTCTCCAGGTACTGCTTGATCTTGTCAAAGTGGCGGTGT 296
Db      719 SerProGly---AlaAlaProArgGlyGlyThrArg-----GlySer 731
QY      295 CGAGCGTGGCCCTTGACAGATGGCGTGGTGGTACATGCTTTCGGCCCTTGATT 236
Db      732 HisAlaAlaArgThrPro-----GlyArgTArgArgHisGlyArgArgProAlaAla 748
QY      235 GGTCTGTCTCCGCAACACAGAGCTCATGAACCTTGACCTGCTTCATCTTCGCT---CTT 179
Db      749 GlyIleLeuProArgArgArg-----ProAlaAlaProAlaAlaProCys 763
QY      178 GCATGTCAGGAGCTCCGAAGGGCAGACGCTCCGGGTCCAGCAGCACCTTATCGTAGA 119
Db      764 ThrValProGlyThrProArg-----AlaProGlyAlaProSerGlySerArgArg 780
QY      118 AGGTGTCAA-----CGCCAGCTTCA 98
Db      781 ArgArgArgArgLeuSerAlaAlaGlyProAlaProLeuArgProHisProProSer 800
QY      97 TGCTTCTG-----CGCGC-----CCAGGT 77
Db      801 ArgLeuAlaGlyAlaAlaGluArgAlaProGluArgArgGlyAlaGlnGlyProProTTP 820
QY      76 CATCAACAGCTTCTGCGCGCGC 53
Db      821 LysAspGlyAlaThrCysCysArg 828

RESULT 9
US-11-182-016-31
; Sequence 31, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US/09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 31
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Tks 118
US-11-182-016-31

Alignment Scores:
Pred. No.: 1.09 Length: 495
Score: 88.00 Matches: 60
Percent Similarity: 30.3% Conserved: 23
Best Local Similarity: 21.9% Mismatches: 83
Query Match: 7.8% Indels: 108
DB: 7 Gaps: 12

US-09-920-953-2 (1-598) x US-11-182-016-31 (1-495)
QY      9 TGCAGACGCGCCACACAGCACCAGAGCGGATGCGGCGCAAGAGCT 68
Db      82 CysGlnAsnGlyHisProAlaHisSerHisAlaThrSerLeuArgArgSerProArgCys 101
QY      69 GTTTGATGACCTGGCGCGCGCAGAGGATGAAGCATGGCGGTGACACCTTCTACGATAA 128
Db      102 -----ProGlySerArgGlyGlnArgArgSer-----LeuCysArg--- 113
QY      129 GGTCTGGTGACCCGAGCTGTGCTTCTTCAGTCCCTTGA----- 173
Db      114 -----ArgLeuProGlySerArgThrGlyHis 122

```

```

QY      174 -----CATGCAAGAGCAGAGATGAAGCAGGTCAAGTTTCATGAGCTT 215
Db      123 GlyHisArgAlaLeuAlaHisAlaProGlyProGluCysGlyGlnCysAlaGlnSer 142
QY      216 CGTGTGTTGGCGAGCAGACCAATACAAAGGCGCCAGCATGTACGACGCACACGCCCATCT 275
Db      143 GlnHisLeuAlaAlaProValGlyAla-----AlaArgArgArgSerProAla 159
QY      276 GGTCAAGGCGCCGCGCTCGACCCAGC----- 302
Db      160 LeuGluValProHisThrGlnProProLeuLeuProAlaProAspMetGluGluCysTTP 179
QY      303 ---CCAATTGCAAGATCAAGCAGTACCTTGGAGA----- 335
Db      180 AlaProAlaProGlnGlnGlyAspLeuProTTPAlaLeuArgTTPGlnGlnLeuAlaLeu 199
QY      336 -----GACGCTGCAAGAGATGGCGTCAACAGCAGATGTGTATCCA 374
Db      200 CysGlnSerGlySerLeuValGlyAlaAlaSerAlaGlyArgGlySerAlaCysGln 219
QY      375 GCA-----CGCGCGGAGTGGTGGAGTCCACCGCGAGAAATTTGACTTNCCTCAA 425
Db      220 AlaGluAspTTPArgTTPArg-TTPTTPThrTTPProSerProSerAlaLysSerProS 239
QY      426 CAACTCGCCACCACTGATTTTCAT----- 451
Db      239 erGlyAlaArgGlnThrProAlaHisPheGlySerLeuLysProLeuLeuAlaAlaP 259
QY      452 -----TAACCCACCCAGCCTGAGCGCTCATTCCTCA 482
Db      259 roThrSerCysSerGlyTTPProArgHisProAlaProAspSerAlaAlaProGlyV 279
QY      483 TCGATTTTGAGCGGCGAGCGCCAGTTGCGAGCGCGCCAGGCGGCCAGGAGCTGCA 542
Db      279 aGln-----ProHisAlaAlaHisAlaProGlyAlaProAlaProAla 294
QY      543 ATCGTTTTCAGCGCTTGTCTGCTGCTG----- 568
Db      294 laAlaValProProArgProAlaAlaPheProProAlaAspGlySerProProSerL 314
QY      569 -----AAGAGC-----CATCAGCCATTTTCG 589
Db      314 euLeuTTPProArgSerCysLeuTyrGlnProPheSer 326

RESULT 10
US-11-087-227-22
; Sequence 22, Application US/11087227
; Publication No. US20050260566A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Timothy J.
; APPLICANT: Malinowski, Douglas P.
; APPLICANT: Taylor, Adriann J.
; APPLICANT: Parker, Margaret R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF CERVICAL DISEASE
; FILE REFERENCE: 046143/287139
; CURRENT APPLICATION NUMBER: US/11/087,227
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 60/556,495
; PRIOR FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-087-227-22

Alignment Scores:
Pred. No.: 1.1 Length: 173
Score: 87.50 Matches: 50
Percent Similarity: 35.5% Conserved: 16

```

```
Best Local Similarity: 26.9%
Query Match: 7.8%
DB: 7
Mismatches: 53
Indels: 67
Gaps: 10
```

US-09-920-953-2 (1-598) x US-11-087-227-22 (1-173)

595	TTGTGTCGGAATAGCTGCTCATGCTCTTCAATGACAGCGGTGGCAACGATTTCGAGG	536		CTCGCGAAC	506
QY					
596					
DB					
42	MetValArgArgPheValThrLeuArg	54			
QY					
535	CTCTGGCGCCCTGGCGCG			CTCGCGAAC	506
DB					
55	AlaCysGlyProProArgValValPheValHisIleProArgLeuThrGlyGlu	74			
QY					
505	TGGCGCTCCCGCCCTCAAAATCGATGGATAGCGCTCAGCGTGGGGTGGTTAAATGAAA	446			
QY					
75	TrpAlaIaPro-----GlyAlaProAlaAlaValAlaLeuVal---	87			
DB					
445	ATCAGTTGGGTGCGCAGTGTGTGGGNAAGTCAAAATTCGTCCGGGTGGAGTCCACCACTC	386			
QY					
88	LeuMetLeuLeuArgSer-----GlnArgLeuGlyGlnProLeu	101			
DB					
385	CGCGCGCTGTGGATCACATCCTGCTTGACGCCCATCTCTTGACGGCTCTCTCAAGT	326			
QY					
102	ProArgArgProGlyHisAspAspGlyGlnArgProSerGlyGlyAlaAla---	118			
DB					
325	ACTGCTTGATCTTGTCAAAGTGGCGGTGGTCCAGCGCTGGCCCTTGACCAAGTGGCGCT	266			
QY					
119	-----AlaAlaProArgArgGly-----	124			
DB					
265	GTGCGTGTGATCATGCTTCGGCCCTTGTATTGGTCTGCTCGGCCCAACACCAAGCTCATGA	206			
QY					
125	-----AlaGlnLeuArgArgProArgHisSer---	133			
DB					
205	ACTTGACCTGCTTCATCTTCTGCTTCGATGTCCAGG-----ACTCGAAGAGG	155			
QY					
134	-----HisProThrArgAlaArgCysProGlyGlyLeuProGlyHisAlaGly	150			
DB					
154	GCAGCAGCTCCGGGTGACCCAGCACTTATCGTAGAGGTGTCAACGCCAGCTTCATGC	95			
QY					
151	GlyAlaAlaProGlyArgGlyAlaAlaGlyArgAlaArgCysLeuGlyProSerAla---	169			
DB					
94	CTTCTGCGCCGCCCAGGT	77			
QY					

RESULT 11

```

US-11-087-227-79
; Sequence 79, Application US/11087227
; Publication No. US20050260566A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Timothy J.
; APPLICANT: Malinowski, Douglas P.
; APPLICANT: Taylor, Adrian J.
; APPLICANT: Parker, Margaret R.
; TITLE OF INVENTION: METHODS AND COM
; TITLE OF INVENTION: DETECTION OF C
; FILE REFERENCE: 046143/287139
; CURRENT APPLICATION NUMBER: US/11/0
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 60/556,49
; PRIOR FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 90
; NUMBER OF FASTSEQ for Windows Versi
; SEQ ID NO 79
; LENGTH: 173
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-087-227-79

```

Alignment Scores:		
Pred. No.:	1.1	Length: 173
Score:	87.50	Matches: 50

Percent Similarity:	35.5%	Conservative:	16
Best Local Similarity:	26.9%	Mismatches:	53
Query Match:	7.8%	Indels:	67
DB:	7	Gaps:	10

US-09-920-953-2 (1-598) x US-11-087-227-79 (1-173)

595	QY	TTGGTGGCAAAATAGCTGATGGCTCTTCAATGACGACGAAGGGCTGGCAACAGATTTCCAGG	536
		:::	
42	Db	MetValArgArgPheLeuValThrLeuArg	54
		:::	
		-----1leArgArg	
535	QY	CTCTGGGGCCCTGGGGCGG	506
		-----CTCGGCAAC	
55	Db	AlaCysGlyProProArgValArgValPheValValHisIleProArgIeuThrGlyGlu	74
505	QY	TGGCGCTCCCGGCTCAAAATCGATGGAATGAGGCTCAGCTGGGTGGTGAATCAAA	446
		-----GlyAlaProAlaAlaValAlaLeuVal	
75	Db	TpAlaAlaPro	87

445	QY	ATCAGTTGGGTGGCGAGTGTGTGGGNAAGTCAAATTGTCGCGGGTGGAGATCCACCACTC	386
		:::	

88	Db	LeuMetLeuLeuArgSer	101
		-----GlnArgLeuGlyGlnGlnProLeu	
385	QY	CGGGCGGTGTGGATCACATCTCTGTGACGCCCATCTCTTCGACGGCTCTCCAAGT	326

102	Db	ProArgArgProGlyHisAspAspGlyGlnArgProSerGlyGlyAlaAla	118

325	QY	ACTGCTTGATCTTGTCAAAGTGGCGGTGGCCAGGCGTGGCCCTTGCACGATGGCGGT	266
		-----AlaAlaProArgArgGly	
119	Db		124
265	QY	GTGCGCTGTATCATGCTTGGCCCTTGTATTGGTGTGCTCCGCCAAACAGAAAGCTCATGA	206
		-----AlaGlnLeuArgArgProArgHisSer	
125	Db		133
205	QY	ACTTGACCTGCTTATCTTCTGCTCTTGCATGTCACGG	155
		:::	
		-----ACTCGAAGAAGG	
134	Db	HisProThrArgAlaArgArgCysProGlyGlyLeuProGlyHisAlaGly	150

154	QY	GCAGCAGCTCCGGGTGCAGCAGCACCTTATCTGTAGAGAGGTGTCAACCGCCAGCTTCATGC	95

151	Db	GlyAlaAlaProGlyArgGlyAlaAlaGlyArgAlaArgCysLeuGlyProSerAla	169

94	QY	CTTTCGCGCGCCGAGT	77
		-----ArgGlyProGly	
170	Db		173

RESULT 12

```

US-11-186-731-5
; Sequence 5, Application US/11186731
; Publication No. US2005025521A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MFI2001-0471RCP1(M)
; CURRENT APPLICATION NUMBER: US/11/186,731
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/077,130
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 7968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-731-5

```

Alignment Scores:
Pred. No.: 1.54 Length: 7968

Score: 87.50 Matches: 59
Percent Similarity: 36.0% Conservative: 26
Best Local Similarity: 25.0% Mismatches: 76
Query Match: 7.8% Indels: 75
DB: 7 Gaps: 13

US-09-920-953-2 (1-598) x US-11-186-731-5 (1-7968)

```
QY 595 TTGTCGCGAAATGGCTGTGGCTCTTCAATGCAGCAAGGCTGGCAACGATTTCAGG 536
Db 64 LeutyArgLeuThrIleLeuAspLeuAlaLeuGlyAspSerGlyGlnTyrValCysArg 83
QY 535 CTCCTGGCGCCCTGGGC-----GCCTCGCAACTGGCGCTCCCGCTCAAA 488
Db 84 AlaArgAsnAlaIleGlyGluAlaPheAlaAlaValGly-----LeuGln 98
QY 487 ATCGATGGAATAGCGCT-----CAGCTGGGGTGGGTAAATGAATCAGTTGG 437
Db 99 ValAspAlaGluAlaAlaCysAlaGluGlnAlaProHiePheLeuLeuArgProThrSer 118
QY 436 GTGCGCAGTTGTGGGNAAGTCAATTCGTGCGGGTGGACTCCACCACCTCGCGCGCGT 377
Db 119 IleArg-----ValArgGluGlySerGluAlaThrPheArgCysArg 132
QY 376 GCTGGATCACATCTGTTGACGCCCTCTCTTGCAGCGTCTCTCCAAGGTACTGCTTGA 317
Db 133 ValGlyGlySerPro-----ArgProAlaValSerTrpSerLysAspGlyArg----- 148
QY 316 TCTTGTCAAAAGTGGCGGTGTGTCAGCGCGTGGCCCTTGACCATGGG---CCTGTGCGT 260
Db 149 -----ArgLeuGlyGluProAspGlyProArgValArg 159
QY 259 CGTACATGCTTCGGC-----CCTTGTATGTT 233
Db 160 ValGluGluLeuGlyGluAlaSerAlaLeuArgIleArgAlaAlaArgProArgAspGly 179
QY 232 CTGCTCGCCAAACACAGACTCATGAACCTTGACCTGCTCTCTCTCTCTCTCTCTCTG 173
Db 180 GlyThrTyrGluValArgAlaGluAsnProLeuGlyAlaAlaSerAlaAlaAlaLeu 199
QY 172 -----CCAGGGACT----- 164
Db 200 ValValAspSerAspAlaAlaAspThrAlaSerArgProGlyThrSerThrAlaAlaLeu 219
QY 163 -----CGAAGAGGCGCAGCTCCGGGTGACGACGACCTTATCTGTAGA 119
Db 220 LeuAlaHisLeuGlnArgArgGluAlaMetArgAlaGluGlyAlaPro----- 236
QY 118 AGGTGTCAACGCCAGCT-----TCATGCTTCTGCGCGCCCGCCAGGTCTATCAA 71
Db 237 ---AlaSerProProSerThrGlyThrArgThrCysThrValThrGluGlyLysHisAla 255
QY 70 ACAGCTTTTGGC-----GCCCGATCCCGCTTCGCGCGTCTCTGTGG 29
Db 256 ArgLeuSerCysTyrValThrGlyGluProLysProGluThrValTrp 271
```

RESULT 13

US-11-072-512-3151

; Sequence 3151, Application US/11072512

; Publication No. US2006002945A1

; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO

; APPLICANT: SUGIYAMA, TOMOYASU

; APPLICANT: OTSUKI, TETSUJI

; APPLICANT: WAKAMATSU, AI

; APPLICANT: SATO, HIROYUKI

; APPLICANT: ISHII, SHIZUKO

; APPLICANT: YAMAMOTO, JUN-ICHI

; APPLICANT: ISONO, YUUKO

; APPLICANT: HIO, YURI

; APPLICANT: OTSUKA, KAORU

; APPLICANT: NAGAI, KEIICHI

; APPLICANT: IRIE, RYOTARO

; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3151
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-072-512-3151

Alignment Scores: 1.45 Length: 354
Pred. No.: 86.50 Matches: 55
Score: 36.2% Conservative: 22
Percent Similarity: 25.8% Mismatches: 65
Best Local Similarity: 7.7% Indels: 71
Query Match: 7 Gaps: 12
DB: 7

US-09-920-953-2 (1-598) x US-11-072-512-3151 (1-354)

```
QY 20 CCACGACGACCA-----CAGAGCGCGGAGCGGATCGCGGC----- 58
Db 137 ProProAlaProAlaProHisTrpAlaSerArgAlaArgSerAlaGlyArgThrArg 156
QY 59 -----GCAAGAAAGCTGTTTGTATGACCTGGCGCGCG 88
Db 157 ArgAlaSerProGlyAlaAlaLeuAlaSerGlySerSerArgArgGluGlyArgCys 176
QY 89 CAGAGCGATGAGCTGGCGGTTGACACCTTCTACGATAAGTGC---TGG---CTGACC 142
Db 177 ArgGlnAlaArgSerProArgSerSerSerThrIleSerArgCysThrTrpGluArgThr 196
QY 143 CGGAGCTGCTGCCCTTCTTCGAGTCCCTGACATGCAAGCAGAGAGATGAAGCAGTCA 202
Db 197 ArgSerThrProGlyPheThrAlaTrpLysThrSerSerAlaArgSerAlaValSer 216
QY 203 AGTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAAGGCGCGAAGCATGTACGACG 262
Db 217 ThrProAlaAlaAlaCys-----GluCysSerArg 226
QY 263 CACACGCCCATCTGTTCAAGGCGCAGCGCTGAGCACCGCCACTTTGACAGATCAGC 322
Db 227 SerSerPro-----ThrSerTrpThr----- 234
QY 323 AGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAGCAGGATGTATCCAGCAGCGCG 382
Db 235 -----ArgSerSerArgLeuGlyAlaAlaGlyPro 244
QY 383 CCGGAGTGTGGAGTCCACCGCGAGAAATTTGACTTNCCTCA----- 424
Db 245 SerAla-----SerProAlaProArgSerLeuProPheProAlaProGlyLeuArgSer 262
QY 425 -----ACAACCTCGCACCCAACTGATTTTCAATTAACCCAAACCCAGCCTGAGCGCT 475
Db 263 GlnArgPheSerThrSerAlaProProArgHisAlaArgProProValAlaAlaGala 282
QY 476 CATTCCATCGATTTTGAGCGGAGCGCCAGTTGCGGAGCGCCCGCGCGG-----GCC 529
Db 283 -----ArgAlaAlaProHisProGlnAlaSerGlyArgLysSer 296
QY 530 CAGGAG---CCTGCAAAATCGTTTGGCCAGCGCTTGTCTGCA 565
```



```
QY 269 GCGTGTGCGTCGTACATGCTTCGGCCCTTGTATTGTTGCTGCTCCGC----- 224
Db ||| :||| ||| ||| ||| ||| :||| :|||
174 rArgAspLysArgProLeuSerGlyProAspValGlyThrProGlnProAlaGlyLeuAl 194
QY 224 ----- 224
Db 194 aSerGlyAlaLysLeuAlaAlaGlyArgProPheAsnThrTyProArgAlaAspThrAs 214
QY 223 -----CAAACACG 216
Db 214 pHisProSerArgGlyAlaGlnGlyGluProHisAspValAlaProAsnGlyProSerAl 234
QY 215 AAGCTCATGAACCTTGACCTCTTCATCTTCTGCTTCTTGTCATGTCAGGGGACTCGAAGAAG 156
Db 234 aGlyGlyLeuAlaIleProGlnSerSerSerSerSerSerSerArgProThrArgAlaAr 254
QY 155 GGCAGCA--GCTCCGGGTGAGCCAGCACCTTATCGTAGAAGGTGTCAA-----CCGCC 105
Db ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
254 gGlyAlaProSerProGlyValLeuGlyProHisAlaSerGluProGlnLeuAlaProPr 274
QY 104 AGCTTCATGCTTCTGCGCGCCGAGGTCAACAGCTTCTTGTGCGCCGCGATCCGCT 45
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
274 oAla---Cys-----ThrProAlaAlaProAlaValProGl 285
QY 44 TCCGCCG 38
Db 285 yProPro 287
```

Search completed: February 27, 2006, 09:18:22
Job time : 17.5 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic acid protein search, using frame_plus_n2p model

Run on: February 27, 2006, 09:13:13 ; Search time 6.8 Seconds
(without alignments)
1454.119 Million cell updates/sec

Title: US-09-920-953-2

Perfect score: 1122
Sequence: 1 ggcgtcgtcgagcagcgcc.....agccattttcgaccacgccc 598

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+n2p.model -DEV=xlp
-Q=/abs/ABSSWEB/spool/US09920953/runat_27022006_065348_20526/app_query.fasta_1
-DB=issued Patents AA -QFMT=fastan -SUFFIX=ra1 -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human0.0.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs02p -USER=US09920953 @CEN 1.1.71 @runat_27022006_065348_20526
-NCPU=6 -ICPU=3 -NO MAP -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:

1: /cgn2_6/ptodata/1/iaa/5 COMB pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB pep.*
4: /cgn2_6/ptodata/1/iaa/PTCUS COMB pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	232	20.7	126	2	US-09-902-540-13031
C 2	136	12.1	345	2	US-09-252-991A-32377
C 3	134.5	12.0	170	2	US-09-252-991A-19880
C 4	134	11.9	663	2	US-09-252-991A-30843
C 5	130.5	11.6	308	2	US-09-252-991A-27249
C 6	129	11.5	1476	2	US-09-252-991A-29427
C 7	126	11.2	235	2	US-09-252-991A-24046
C 8	125.5	11.2	394	2	US-09-252-991A-19344
C 9	124	11.1	312	2	US-09-252-991A-19787
10	122	10.9	726	2	US-09-252-991A-20675
11	121.5	10.8	204	2	US-09-252-991A-17837
12	121.5	10.8	351	2	US-09-252-991A-18476

13	121	10.8	248	2	US-09-252-991A-20161	Sequence 20161, A
14	121	10.8	686	2	US-09-252-991A-20509	Sequence 20509, A
C 15	120	10.7	219	2	US-09-252-991A-23215	Sequence 23215, A
C 16	119.5	10.7	209	2	US-09-252-991A-24725	Sequence 24725, A
17	119.5	10.7	266	2	US-09-252-991A-32478	Sequence 32478, A
18	119.5	10.7	720	2	US-09-252-991A-32006	Sequence 32006, A
19	119	10.6	222	2	US-09-252-991A-26487	Sequence 26487, A
C 20	118.5	10.6	247	2	US-09-252-991A-26899	Sequence 26899, A
21	118	10.5	536	2	US-09-252-991A-20771	Sequence 20771, A
22	118	10.5	565	2	US-09-252-991A-20122	Sequence 20122, A
23	117.5	10.5	273	2	US-09-252-991A-30433	Sequence 30433, A
24	117	10.4	153	2	US-09-252-991A-20543	Sequence 20543, A
25	117	10.4	204	2	US-09-252-991A-21783	Sequence 21783, A
C 26	116.5	10.4	191	2	US-09-252-991A-25365	Sequence 25365, A
27	116.5	10.4	326	2	US-09-252-991A-18751	Sequence 18751, A
C 28	116.5	10.4	335	2	US-09-252-991A-23674	Sequence 23674, A
29	116.5	10.4	977	2	US-09-252-991A-16655	Sequence 16655, A
C 30	116	10.3	160	2	US-09-252-991A-30765	Sequence 30765, A
31	116	10.3	297	2	US-09-252-991A-29217	Sequence 29217, A
32	116	10.3	369	2	US-09-252-991A-20790	Sequence 20790, A
33	115.5	10.3	172	2	US-09-252-991A-20172	Sequence 20172, A
34	115	10.2	266	2	US-09-252-991A-19128	Sequence 19128, A
35	115	10.2	681	2	US-09-252-991A-21837	Sequence 21837, A
36	114.5	10.2	143	2	US-09-252-991A-25813	Sequence 25813, A
37	114.5	10.2	168	2	US-09-252-991A-29614	Sequence 29614, A
C 38	114.5	10.2	173	2	US-09-252-991A-32359	Sequence 32359, A
C 39	114.5	10.2	200	2	US-09-252-991A-24828	Sequence 24828, A
40	114.5	10.2	474	2	US-09-252-991A-16788	Sequence 16788, A
41	114	10.2	320	2	US-09-252-991A-24634	Sequence 24634, A
42	114	10.2	480	2	US-09-252-991A-31470	Sequence 31470, A
C 43	114	10.2	554	2	US-09-252-991A-28232	Sequence 28232, A
44	114	10.2	697	2	US-09-252-991A-24009	Sequence 24009, A
45	114	10.2	1706	2	US-09-252-991A-31760	Sequence 31760, A

ALIGNMENTS

RESULT 1

US-09-902-540-13031
; Sequence 13031, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13031
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13031

Alignment Scores:
Pred. No.: 3,43e-16
Score: 232.00
Percent Similarity: 56.1%
Best Local Similarity: 41.5%
Query Match: 20.7%
DB: 2
Gaps: 2

US-09-920-953-2 (1-598) x US-09-902-540-13031 (1-126)

QY 37 ACGGCGAGCGGATCGCGCGAAGAGCTGTTTGTAGCTGGCGCGCGAGAGGC 96
DB 4 ThrAlaGlu-----LysSerValtyrGluGlnLeuGlyGlyGluProAla 18

```
QY 97 ATGAAGTCGGCGTTGACACCTTCTACGATAAGTGTGCTGGTGTGACCCGAGCTGCTGCC 156
Db 19 MetAlaAlaValGluValPheTyrArgLysValLeuAlaAspHisSerHis 38
QY 157 TTCTTCAGTCCCTGGACATGCAAGACAGAGATGAAGCAGGTCAAGTTCATGAGCTTC 216
Db 39 PheGluAspValAspMetGluArgGlnAlaAlaLysGlnLysAlaPheLeuThrMet 58
QY 217 GTGTTTCGGCGAGCAGACCAATACAAGCGCGAGCATGTACAGCGCACCGCCCATCTG 276
Db 59 ValThrGlyGlyProValHisTyrSerGlyLysAspMetArgAlaGlyHisAlaProLeu 78
QY 277 GTCAAGGCCCGCCCTGGACCCAGCCGCTTTCACAGATCAAGCAGTACCTTTGGAGAG 336
Db 79 ValLys---ArgGlyLeuAsnAspSerHisPheAspAlaValAlaGlyHisLeuLysAla 97
QY 337 ACGTTCAGAGATGGCGGTCAAGCAGGATGTGATCCAGCAGCGCCGCGGAGTGGTGAG 396
Db 98 ThrLeuGluGluLeuGlyValAlaAlaProLeuValAlaArgValMetThrIleAlaGlu 117
QY 397 TCACCCCGC 405
Db 118 SerAlaArg 120

RESULT 2
US-09-252-991A-32377
; Sequence 32377, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32377
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32377

Alignment Scores:
Pred. No.: 8.49e-06 Length: 345
Score: 136.00 Matches: 70
Percent Similarity: 34.8% Conservative: 10
Best Local Similarity: 30.4% Mismatches: 64
Query Match: 12.1% Indels: 86
DB: 2 Gaps: 10

US-09-920-953-2 (1-598) x US-09-252-991A-32377 (1-345)
QY 539 CAGCTCTGGCGCCCTGGCGCGCTGGCACTGGCTGCC---GCTCAAAATCGA 483
Db 101 GlnGlyProGlyGlyProGlyArgAspArgGlnValArgLeuProAlaAlaProGlyArg 120
QY 482 TGAATGAGCCTCAGGCTGGGGTGGTTAATGAAATCAGTTGGTGGCGAGTTCTTG 423
Db 121 ProSerArgArgGln-----SerArgLeu 128
QY 422 GGNAAATCAATTCGTCCGGGTGGAGTCCACCACTCCGGCGGTCTGGA----- 371
Db 129 GlnArgHisGlyLeuSerArgCysProLeu-ProLeuArgArgProSerProAla 148
QY 370 -----TCACATCC 363
Db 148 aTrpArgGlnProProIleGluLeuGlyAlaValArgLeuArgProGlnArgArg 168
QY 362 TGCTTGACGCCATCTCTTGACGGCTCTCTCCAGGCTACTGCTTGATCTTGTCAAAGTGG 303
```

```
Db 168 oAlaGlnArgProAlaValAlaAla----- 176
QY 302 CGTGGT-----CCAGGCGGTGGCTTGCACAGATGGCGCTGTGCGTGCATCATG 252
Db 177 -GlyGlyGlnArgGlnProGlyArgAspProAlaGluHisLeuArgProArgArgPro-- 195
QY 251 CTTCCGCCCTTGATTGGTCTGCTCCGCCAAACACCAAGCTCATGAATTGACTGCTTC 192
Db 196 -----GlyLeuLeuArgArgProArgArg-----ProAlaGln 206
QY 191 ATCTTCTGCTTTTCATGT-----CCAGGGACTCCAAGAAG 156
Db 206 nProGlyArgLeuAlaSerGlyArgGlyAlaGlyGlyAlaGluProGlySerArgArgAr 226
QY 155 G-----CGACGAGC 147
Db 226 gGlnValProGlyArgArgArgProPheArgSerProAlaGlyAlaAspArgAlaVa 246
QY 146 TCCGGGTGACCCAGCACCTTATCGTAGAAGGTGTCAACGCCAGCTTCATGCTCTTCGCG 87
Db 246 lProGlyGluProArgProGlyProArgArgArgArgProGluGlnArgProArgArgHi 266
QY 86 CGCCCGCAGTCAAT---CAAACAGCTTCTTCCGCCCGCATCCCGCTTCCCGCTCTCTGTG 30
Db 266 sArgProAlaHisGlyProGlyAlaGly-TyrProAlaAlaProLeuArgArgAlaGlyG 286
QY 29 GTGCTGGTGGCGCGCTCTGCAGGCGAG 4
Db 286 lAlaThrArgHisArgLeuArgGln 294

RESULT 3
US-09-252-991A-19980
; Sequence 19980, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19980
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19980

Alignment Scores:
Pred. No.: 9.39e-06 Length: 170
Score: 134.50 Matches: 68
Percent Similarity: 38.3% Conservative: 9
Best Local Similarity: 33.8% Mismatches: 45
Query Match: 12.0% Indels: 79
DB: 2 Gaps: 15

US-09-920-953-2 (1-598) x US-09-252-991A-19980 (1-170)
QY 524 CTGGGGCGCTCGGCAACTGGCGCTCCCGCTCAA-----AATCGATGAATGAGCGC 471
Db 14 ProGlyArgArgAsnArgArgAlaAlaProAlaAlaAlaGlyArgArgSerAlaArg 33
QY 470 TCAGGCTGG-----GTTGGGTTAATGAAATCAGTTGGTGGCGAGTTGTTGGGNAAG 417
Db 34 SerGlyTrpProCysGlyTrp-----Arg-TrpSerHisProCysTrp----- 47
QY 416 TCAAAATTCGTCCGGGTGGAGTCCACCACTCCCGCGCGTGTGGATCCATCTGCTTG 357
```

Db 48 -GlnHisArgArgArgProSerArgArg-----SerArgProAlaAla 64
 QY 356 AGCCCATCTCTGAGCGCTCTCTCAAGGTACTGCTTGAATCTTGTCAAGTGGCGGTGG 297
 Db 64 aArgPro-----SerGlyGlyAl 70
 QY 296 TCCAGGCGTGGCCCTTGACAGAT-----GGCGGTGTGCGTGTACATCTTTCGG 246
 Db 70 alaIleArgArgProValProAspGlyGlnProGlyArgArgArgAsnAlaCys----- 88
 QY 245 CCCTTGATTTGCTGCTCGCCCAACACGAGACTCATGAATTCACCTGCTTCATCTTC 186
 Db 89 -----SerThrArg----- 91
 QY 185 TGCTCTTGCATGTCAGGACTCGA-----AGAGGCGACAGC 147
 Db 92 -----LeuProGlyArgArgArgPheProTrpArgProThrArgArgSerAl 108
 QY 146 TCGGGTCTAG-----CCAGCCTTATCTGAGA-----AG 117
 Db 108 aProGlySerArgThrGluArgAlaProSerProAlaArgArgGlySerArgSerAr 128
 QY 116 GTGTCAACCGCCAGCTTTCATGCTTCTGCGCCGCCAGGTCTCAACACAGCTTCTTGGC 57
 Db 128 gArgArgProAlaAla-----ArgArgGlyThrLeuProCysProAlaCysSe 144
 QY 56 CCGCATCCCGTTCGCGC-----CGTCTCTGT-----GGTCTGCTGCGCCGCTGTC 10
 Db 144 r-AlaSerArgAsnArgSerArgSerCysSerArgGlySerAlaGlyArgSerCys 163

RESULT 4

US-09-252-991A-30843
 ; Sequence 30843, Application US/09252991A
 ; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 30843
 ; LENGTH: 663

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-30843

Alignment Scores:
 Pred. No.: 1,77e-05 Length: 663
 Score: 134.00 Matches: 53
 Percent Similarity: 35.7% Conservative: 17
 Best Local Similarity: 27.0% Mismatches: 71
 Query Match: 11.9% Indels: 55
 DB: 2 Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-30843 (1-663)

QY 512 CGGCACTGGCGCTCCCGCTCAAAATCATGATGG-----AAT 477
 Db 45 ArgArgValProIleArgCysAlaAsnAlaTrpProGlyArgProMetSerSerThrSer 64
 QY 476 GAGCGCTCAGGCTGGGGT-----TGGGTTTAATGAAAT 444
 Db 65 ArgArgProGlyTyrSerProAlaValProAlaGlyAlaCysCysTrpIlyThrArgAsn 84
 QY 443 CAGTTGGGCGCAGTGTGTGGNAGTCAANTGCTCGCGGGTGAGTCCACCACTCCG 384
 Db 85 ValAlaGlyArgSerAlaThrAspAlaTrpSerSer-----AlaProAlaPro 100

QY 383 GCGGGTCTCTGATCACAATCTCTGTTAGCGGCATCTCT-----TGCAGCTCTCT 333
 Db 101 AlaAsnCys-----CysCysLeuPheProAlaGlyProSerProAlaSerProAla 117
 QY 332 CCAAGGTACTGCTTGTCTTCAAGTGGCGGTGGTCCAGGCG-----TGGGCC 282
 Db 118 ProAlaAlaCysArg-----ArgTrpProArgAlaAlaCysHisTrpPro 132
 QY 281 TTGACCATGAGCGGTGTGCGTGTACATGCTTTCGCCCC-----TTGATTTGGTCTGCT 228
 Db 133 AlaSerAlaTrp-----TrpTrpLeuAlaProAlaArgCysCysTrpProAla 148
 QY 227 CGCCAAACACGAGCTCATGAACCTTGACCTGCTTCATCTTCTGCTTGTGATGTCAGG 168
 Db 149 ProPro-Ala-----ProAlaSerAlaGlyArgAlaCysCysAlaSe 162
 QY 167 GACTCGAAGAGGGCAGCAGCTCGGGTGCAGCAGCCTTATCTGTAGAGGTGTCAACC 108
 Db 162 rProAsnArgArgArgArgGluProTrpProProSerProTrpAlaSerArgAla---G1 181
 QY 107 GCCAGCTTTCATGCTTCTGCGCCGCCAGGTCTCAACACAGCTTCTTGGCCCGCATCCC 48
 Db 181 yProAlaSerCys-----GlyArgPro-----ProAlaCysSerProValAla 195
 QY 47 GCTTCCGCGCTCTGTGCTGTGCTGTGCGCGCTGCGCGCTGCGAGGCG 2
 Db 195 aThrAlaProThrAlaThrCysSerProProSerProAlaArgSerAla 210

RESULT 5

US-09-252-991A-27249

; Sequence 27249, Application US/09252991A
 ; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 27249
 ; LENGTH: 308

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-27249

Alignment Scores:
 Pred. No.: 3.14e-05 Length: 308
 Score: 130.50 Matches: 77
 Percent Similarity: 36.6% Conservative: 13
 Best Local Similarity: 31.3% Mismatches: 81
 Query Match: 11.6% Indels: 75
 DB: 2 Gaps: 17

US-09-920-953-2 (1-598) x US-09-252-991A-27249 (1-308)

QY 593 GGTGCAAAATGGCTGTGATGGCTCTTCAATGCAGCAAGGCTGGCAACGATTTGCAGGCT 534
 Db 21 GlyAlaGlyProGlyArgGlyGlySer---GlyProGlyArgAlaGlyArgArgSerIle 39
 QY 533 CTGGGCGCCCTGGCGCGCTCGGCAACTGCGCTCCCGCTCAAAATCGATGGAATGAG 474
 Db 40 ProProAlaProArgArgGlyProArgLeuAlaArgProSerArgGlyArgGlyArgThr 59
 QY 473 CGC-----TCAGGCTGGGGTTCGGTT-----AATGAAATCAGTTG 438
 Db 60 ArgAlaProGlyArgCysCysSerGlyTrp---TrpSerThrGlySer-ProMetAlaPr 78

```

QY 437 GGTGGCGAGTGTGGNAGTCAATTCCT-----CGGGGTGGACTCCACACTCCG 384
Db 78 oValArgSerAlaCysArgGlyThrSerArgProValArgSerTrpProGlyProAl 98
QY 383 GCGGCGTGTGATCATCTCTCTGACGCT-----CCATCTCTTGC 342
Db 98 aGlyA-gAlaGlyGlyTrpGlyArgArgGlyProArgSerValProThrVa 118
QY 341 AGCGTCTCTCAAGGTACTCTTGATCT-----TGTCAAAGTGGCGGTGCTCC 294
Db 118 lAlaSerValAlaGlyProSerArgSerGlyAlaGlyProAlaArgAlaAlaGlyPr 138
QY 293 AGCGGTGGCCCTTGACCA----- 275
Db 138 oGlyAlaAlaProCysProGlyProGlyArgGlySerGlyAlaAlaArgHisArgAr 158
QY 274 -----GATGGGGTGTGGTGTGATCATCTCTCGGCCCTTGATGTGCTCCG 225
Db 158 gGlyArgArgProGlyArgArgSerArgTrpCys-----ProCysAlaGly---SerAr 175
QY 224 CCAACACAGAGTCAAGACTTGACCTGCTTCATCTCTGCTCTTGCACTCCAGGCAC 165
Db 175 gAlaArgArgProSer-----GlyCysThrGlyCy 185
QY 164 TCGA-----AGAGGGCA-----GCAGTCCGGGTGAGCCAGCACCTTA 126
Db 185 sArgProArgLeuProArgArgAlaGlyArgA-gAlaAlaGlyGlyArgProPro----- 203
QY 125 TCGTAGAGTGTCAACCGCCAGCTTCATCCCTCTGCGCGGCCAGGTCAATCAA----- 71
Db 204 -----CysCysProGlyAla-----ProGlyGluArgLysAr 215
QY 70 ----ACAGCTTCTTGCGCCGCGATCCGCTCTCGCGCTCTCTGTTGTTGGTGGCGCG 15
Db 215 gSerThrGluSerSerAlaArg---ProAlaPro-ArgProCysGlyGlySerGlyArgG 234
QY 14 TCTGCGAGCGCGC 1
Db 234 lyAlaArgHisArg 238

```

RESULT 6

```

US-09-252-991A-29427
; Sequence 29427, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29427
; LENGTH: 1476
; TYPE: PR1
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29427

```

```

Alignment Scores:
Pred. No.: 8.18e-05 Length: 1476
Score: 129.00 Matches: 74
Percent Similarity: 38.0% Conservative: 10
Best Local Similarity: 33.5% Mismatches: 91
Query Match: 11.5% Indels: 46
DB: 2 Gaps: 13

```

```

US-09-920-953-2 (1-598) x US-09-252-991A-29427 (1-1476)

```

```

QY 9 TGCAGAGCGCGCCACCAAGCAGCACAGAGCGGCGGAAGC-----GGGATCGCG 56

```

```

Db 492 CysArgArgAlaHisArgGlnHisArgGlnAlaAlaAspAlaLeuGlyGlnArg 511
QY 57 GCGCAAGAGCTGTTGATGACCTGGCGCGCAGAAAGCATGAAGCTGGCGTTCCACAC 116
Db 512 ThrGlnLeuSerArg---ArgProGlyGlnLeuArgArgAlaProGlyHisArgAlaHis 530
QY 117 CTTCTACGATAGGTGCTGGCTGACCCGAGTGTGCTCTCTTCCAGTCCCTGACAT 176
Db 531 LeuProGlnLeuGlyAlaAla---ValGlyGlyAlaGlyLeuArgArg-----GlyHis 547
QY 177 GCAAGAGCAGAAGTCAAGCAGTCAAGTTCATGAGCTTCGTTGTTGGCGGAGCACCA 236
Db 548 ArgProGlyArgTrpProValGlyLeuValArg-----ArgArgLeuPro 562
QY 237 ATA-----CAAGGCGGAGCATGTACGACGACACAGCCCATCTGCTCAAGGCGCCACGG 290
Db 563 AlaGlyArgArgGlyThrArgGlnGlyArgThrArgArgProGlyProGlyProAla 582
QY 291 CTTGGA-----CCACGCCCA-----CTTTGACAAGATCAAGCAGTA 326
Db 583 ProGlyAlaGlyAlaAspArgProProAlaPheLeuLeuSerGlyAlaAlaArg 602
QY 327 CTTGAGAGAGCTCCAAAGAGATGGCGTCAA-----GCAGATGTGATCCAGCAGC 380
Db 603 Pro---ArgArgAlaGlyProAspArgGlnProProAlaGlyProAspProGlyArg 621
QY 381 CGCGGAGTGTGGAGTCCACCCGC-----GACGAATTTGACTTNCACCAACA 428
Db 622 ArgHisArgGlyAlaVal---ThrArgCysGlyAlaGlyThrGluAlaGlyValProArgPr 641
QY 429 CTGCGCACCAACTGATTTTTCATTACCCCAACCCACAG----- 465
Db 641 oProGlnProAlaAspGlyAlaThrAlaAlaAspGlnGlnGlyArgAspProGlySerHi 661
QY 466 ----CTGAGCGCTCATCTCATCGATTTTGACGGGAGCGCCAGTTGCGAGCGGCC 521
Db 661 sProProGlyArgAspAlaArg-----AlaThrValArgProArgPr 676
QY 522 AGGGGCGCGAGGAGCGCTGCAATCGTTTGCAGCCCTTGTGCTGATTAAGAGGATCAG 580
Db 676 oSerArgProAlaGly-GlnTyrHisProProAlaArgValAlaGlyLysArgHisArg 695

```

RESULT 7

```

US-09-252-991A-24046
; Sequence 24046, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24046
; LENGTH: 235
; TYPE: PR1
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24046

```

```

Alignment Scores:
Pred. No.: 8.54e-05 Length: 235
Score: 126.00 Matches: 47
Percent Similarity: 39.2% Conservative: 18
Best Local Similarity: 28.3% Mismatches: 58
Query Match: 11.2% Indels: 43
DB: 2 Gaps: 10

```

US-09-920-953-2 (1-598) x US-09-252-991A-24046 (1-235)

```

QY 482 TCGAATGACGCTCAGGC---TGC-----GGTTGGTGAATGAAATCATCAG 441
Db 26 TTPAspGlyArgSerGlyArgTrpSerArgTyrCysAlaTrp-----40
QY 440 TTGGGTGCGCAGTTGTGGGNAAGTCAAAATTCGTGCGGGTGTGACTCCACCACTCCGGG 381
Db 41 ---GlyCysProSerValAlaProThrArgTrpSerArgGlyCysSerArgSerProPro 59
QY 380 GCGTGTGCTGCATCAGTCTGTCAGCCCATCTCTTGACGGCTCTCTCCAAAGGTACTGC 321
Db 60 CysAlaTrpAlaSerSerAlaIleThrProTrpProArgThrArgSerProSer-----77
QY 320 TTGATCTTGTCAAAGTGGCGGTGTCACGCGGTGCGCCCTTGACCAAGATGGCGGTGTCG 261
Db 78 -----ArgArgTyrThrTrp---ArgSerTrp-----CysArgTrpGlyCysArg 91
QY 260 TCGTATGCTTGGGCCCTTGATTGCTGTCTGCGCCAAACACAGCAGTCTCATGACTTG 201
Db 92 -----ThrProProPro-Thr-----96
QY 200 ACTGCTTCTATCTTCTGCTTTCGANGTCCAGGACTCGAAGAGGCGCAGCTCCCGG 141
Db 97 -----AlaSerAlaSerIleSerAlaProAlaAlaCysSerLysHisAlaAlaProGl 114
QY 140 TCAGCAGCAGCACTTATCGTAGAGGTGT-----CAACCGCCAGCTTTCATGCT 93
Db 114 yValSerAlaSerAlaSerAlaArgCysAlaCysSerSerProGlySerSerGlyGl 134
QY 92 TCTGCGCGCGCGAGTCAACAGCTTCTTGGCGCCGATCCCGCTTCGCGGCTCTCT 33
Db 134 yCysArgArgProSerSerAlaCysSerSerThrAla---ThrProArgProThrGlyArg 153
QY 32 GTGGTCTGTGTGCGCG 17
Db 153 gtrpProArgTrpPro 158

```

RESULT 8

```

US-09-252-991A-19344
; Sequence 19344, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19344
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19344

```

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
17	0.000117	394	68
116	125.50	68	16
	31.8%	Conservative:	76
	25.8%	Mismatches:	104
	11.2%	Indels:	11
	2	Gaps:	

US-09-920-953-2 (1-598) x US-09-252-991A-19344 (1-394)

```

QY 17 CGGCCACGACGACGACGAGCGG-----CGG 43
Db 116 ArgProGlyAlaProGluProArgGlyThrProProValGlyProGlySerLeuSerArg 135

```

```

QY 44 AAGCGGGATGCGGCGCGCAAGAGCTGTTTGTATGACTGCGGCGG-----CGCAG 91
Db 136 ArgLysProAlaGly-AspLeuAla-----ProProArgGlnLeuAlaAspArgPr 152
QY 92 AAGGCATGAAGCTGCGGCTTGACACCTTCTACGATAAGTGTGCTGCTGACCGGAGCTGC 151
Db 152 oAlaHisProProGlyGlySerHisLeuGlnLeuProGlyAlaGlyProProGlyArgVa 172
QY 152 T-----GCCCTTCTTCGA-----164
Db 172 IArgProAlaValSerLeuProProAlaValPheArgArgLeuHisGlnProAlaValAr 192
QY 165 -----GTCCCTGACATGCAAGAGCAGAGATGAGCAGGTCAAGTCAAGTTCAGCTTCG 217
Db 192 gArgProLeuProGlyHisAlaAlaAla-----AlaGlyArgThrHisProGlnAl 209
QY 218 TGTT-----TGGCGGAGCAGACCAAT 238
Db 209 aValProProAlaLeuSerArgArgProAlaGlyAlaProGlyArgArgGlnProAr 229
QY 239 ACAA---GGGCGGAAGCATGTACGACGACGACGCGCCATCTGTGTCAGGCGCCAGCGCTCG 295
Db 229 pGlnProAspProProProAlaArgProArgLeuProAlaLeuAlaGlyProArgProGl 249
QY 296 ACCACGCGCCTTTGCAAGATCAAGCATCAAGTACCTTGGAGAGACGCTGCAAGAGATGGCG 355
Db 249 yArgProProThrAlaHisGluPheAlaAspProAlaThrProProAlaArgGlyArgAr 269
QY 356 TCAA-----359
Db 269 gGlnLeuProAlaThrGlnGlyProProAlaAlaArgProGlyAspLeuProProGlySe 289
QY 360 -----CGAGATGTGATCCAGCAGCAGCGCGCGAGTGTGTGAGTC-----398
Db 289 rGlyArgAlaValAspProGlyHisArgArgAlaAlaArgLeuPheArgAlaLeuGlyLe 309
QY 399 -----CACCGGAGCAGCAATTTGACTTNNCCCAACA 427
Db 309 uProSerArgValGlnGluValAspArgProHisProArgArgVal-----324
QY 428 ACTGCGCGCCCAACTGATTTTCATTAACCAACCCCGCTGAGCGCTCATTCATCGAT 487
Db 325 -----ProAlaProGlyGlySerLeuLeuSerPr 335
QY 488 TTTGAGCGGAGGAGCGCCAGTTGCGGAGCGCGCGCGGCGCGGAGGAGCTGCAATCGT 547
Db 335 oThrProGlyAspGluAlaArgCysAlaValGlyArgAlaProTrpArgThrAlaAla 355
QY 548 TTGCCAGGCC 557
Db 355 aAlaArgPro 358

```

RESULT 9

```

US-09-252-991A-19787
; Sequence 19787, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19787
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

```

US-09-252-991A-19787

Alignment Scores:

Pred. No.: 0.000155 Length: 312
Score: 124.00 Matches: 59
Percent Similarity: 37.7% Conservative: 13
Best Local Similarity: 30.9% Mismatches: 73
Query Match: 11.1% Indels: 46
DB: 2 Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-19787 (1-312)

```
QY 9 TGCAGACGCGCCACACAGACAGACGCGGGAAGCGGATGCGGCGCAAGAGCT 68
DB 39 CysArgArgProGluGlnHisAlaProHisArgGlyAspGlyArgArgAlaTrpArg--- 57
QY 69 GTTGTAGACTGGCGCGCGCAGAGGCATGAAGCTGGCGGTTCACACCTTCTACGNATA 128
DB 58 -----GlyHisArgProSer----- 63
QY 129 GGTGCTGGTGACCCGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAA 188
DB 64 GlyLeuProArgProGlyArg-----LeuArgAlaSerAlaHisArgArgAlaGly 80
QY 189 GATGAACGAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGC-----AGACCAATA 239
DB 81 HisArgAlaGlyGlnArgHisAlaLeuProAlaTrpArgThrAlaArgIleArgProAla 100
QY 240 CAAGGCGGAGCATGTACAGCGCACAGGCCA-----TCT 275
DB 101 AlaGlyProValAlaAlaThrArgGlnAlaProArgArgAlaLeuHisAlaProGlyAla 120
QY 276 GGTCAAGCGGCACCGCTGGACACCGCTTGGACAGTCAAGCAGTACCTTGGAGA 335
DB 121 GlyArgGlyArgArg-----AlaProValArgArgAspProAlaThrProGlyThr 137
QY 336 GACGCT-----GCAAGAGATGGCGTCAAGCAGGATGTGATCCAGCAGCG 380
DB 138 GlyThrAlaAlaLeuLeuHisAlaArgPheGlyHisLeuAla-----HisArg 153
QY 381 CGCGGAGTGGTGAAGTCCACCGCGAGCAATTTGACTTCCCACTGCGGCGACCCAA 440
DB 154 ProGlyThrGlyProAlaAlaGlyAlaArgValLeuArgArgProArgLeuArgProGln 173
QY 441 CTGATTTTC---ATTAAACCAACCCAGCTGAGCGCTCATTCATCGATTTTGAGCGGG 497
DB 174 ArgLeuHisArgLeuHisProAla-----GlyArgArgProArgSerAlaAlaGly 190
QY 498 GAGCGCGAGTTGCGAGC---GCGCCCGAGGGG 527
DB 191 ArgArgGlnGlyProAlaArgLeuProArgGly 201
```

RESULT 10

US-09-252-991A-20675
; Sequence 20675, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20675
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20675

Alignment Scores:

Pred. No.: 0.000349 Length: 726
Score: 122.00 Matches: 74
Percent Similarity: 32.1% Conservative: 6
Best Local Similarity: 29.7% Mismatches: 74
Query Match: 10.9% Indels: 95
DB: 2 Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-20675 (1-726)

```
QY 2 CGTGTGCTGCAGC-----CGGCCACACACACACAGCGGCGGAGCGGGATGG 55
DB 299 ArgAlaLeuArgThrGluArgHisProProAspProGlyArgHis-GlyProProAla 318
QY 56 GGCGCAAGAAGCTGTTTGATGACCTGGCGCGCGCAGAAGG-----CATCAAGC 103
DB 318 g-----ProAlaAlaArgArgArgAlaAlaAlaValGlyGluAl 331
QY 104 TGSC-----GGTTGACACCTTCTACGATAAGTGTGGC-----TGACCCGAGC 148
DB 331 aGlyAlaAlaGlyGlnGlyProArgArgThrGlyAlaAlaAlaArgThrGlnSerProGly 351
QY 149 TGCTGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTCA 208
DB 351 rAlaGlySerAlaAlaLeuArgAlaHisArgArgAlaGluGlySerAla-----AlaG 369
QY 209 TGAGCTTCGTGTT-----TGG----- 224
DB 369 yGluLeuArgAlaArgProGlyProTrpProAlaAlaGlnGlnProAlaSerAlaAlaPr 389
QY 225 -----CGGAGCAGACCAATACAAAG 244
DB 389 oAlaProGlyGluGlyArgGlyThrAlaArgAlaAlaArgArgGlnAlaAlaArgGlnAr 409
QY 245 GCCGAAGCATGTACGAGGACACCGCCCACTGTGTCAAGGCCACGCGCTGGACCCGCC 304
DB 409 gProThrAlaValArgThrAspArgGluAspGlnGlyArgProArgProProProPr 429
QY 305 ACTTTGACAA-----GATCAA-----GCAGTACCTTGGAGAGACGCTGCAAG 346
DB 429 oProAlaGlnProGluAspGlnProAlaProAlaAlaAlaProGlyArgAspAlaAlaAr 449
QY 347 AGAT----- 350
DB 449 gAspAspProGlnArgThrHisGlyThrAlaProAlaGluGlyAlaAlaGlnProGlnAr 469
QY 351 -----GGCGTCAACGAGATGTGATCCAGCAGCGCGCGGAGTGGTGGAGT 397
DB 469 gGlnProAspHisGlyArgHisGlnProGlyAspProGlyValLeuProArgGlyGlyAl 489
QY 398 CCACCCGCGACGAATTTGACTTCCCAACCACTGCCCACTGATTTTTCATTAAACCC 457
DB 489 aArgProArg-----GlnProArgAlaArgGlyArgHisGlyGlnPr 503
QY 458 AACCCCGAGCTGAGCGCTCATTCATCGATTTTGGCGGGAGCGCGCAGTTGCCGAGCGC 517
DB 503 o-----HisGlyArgArgHisLeuProAla 512
QY 518 GCCCGAGGGGCCAGGAGCGCTGCA 542
DB 512 aGlnArgGlyGluProAlaLeuArg 520
```

RESULT 11

US-09-252-991A-17837
; Sequence 17837, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17837
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17837

Alignment Scores:
Pred. No.: 0.00244 Length: 204
Score: 121.50 Matches: 60
Percent Similarity: 34.6% Conservative: 15
Best Local Similarity: 27.6% Mismatches: 77
Query Match: 10.8% Indels: 65
DB: 2 Gaps: 14

US-09-920-953-2 (1-598) x US-09-252-991A-17837 (1-204)

QY 5 TGCCTGCAGCGCGCCACAGCAGCAGCGCGGATGCGGCGCAAGA 64
DB 7 CysSerSerThrArgProThrProThrTrp-----ProSerAlaIaen 21
QY 65 AGCTGTTTGCATGACCTGCGCGCGGAGAGGATGAGCTGGCGTTGACACCTTCTACG 124
DB 22 SerMetAlaThrAlaThrProPheProAlaAlaSerTrpArgThr-----Thr 39
QY 125 ATAAGTGCTGG-----CTGACCCGCGAGCTGC----- 151
DB 40 SerArgCysAlaProAlaThrAspArgSerCysSerThrAlaThrSerGlyIleArg 59
QY 152 TGCCTTCTTCAGTCCCTGACATGCAGCAGCAGAGATGAGCAGGTCAAGTTCATGA 211
DB 60 CysGlyThrSerArgProTrp---AlaGlySerArgProProProSerSer----- 76
QY 212 GCTTCGTGTTGGCGGAGCAGCAATACAGGCGCGGAGCATGTACGACGACACGCC 271
DB 77 -----ArgGluProGluProCys-----ArgAlaPro 85
QY 272 ATCTGTCAAGGCGCCAGCTGACACCGCCACTTTCAGCAAGATCAAGCAGTACCTTG 331
DB 86 ProTrpSer-----AlaAlaThr-----AlaAlaThrCys 95
QY 332 GAGAGCGCTGCAGAGATGGCGTCAAGCAGATGTGTATCCAGCAGCGCGCGAGTGG 391
DB 96 ProArgProCysSerAlaThrThrCysSer-----ProProSerTrp 109
QY 392 TGGAGTCCACCGCGAGATTTGACTTNCACCAACTGCGCACCACCACTGATTTTCAT 451
DB 110 ThrLeuProThrProGlySerAlaAlaAlaProAlaCysAlaSerGlyIle----- 126
QY 452 TAACCAACCCAGCTGAGCGCTCATTCATGATTTTGGCGGAGCGCCAGTT----- 508
DB 127 -----SerProAlaThrSerAla---AlaAlaThrTrpProCysGlyArgProPro 143
QY 509 -----GCCGAGCG 547
DB 144 ArgSerProArgArgGlyTrpSerGluSerMetArgTrpCysTrpGlnProAla----- 161
QY 548 TTGCCAGCCTTCTGCATTGAGAGCCATCAGCCATTTTCGCCACCAAGCC 598
DB 162 ---ProAlaThrSerAlaAlaArgProProArgProGlySerArgAla 177

RESULT 12
US-09-252-991A-18476
; Sequence 18476, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18476
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18476

Alignment Scores:
Pred. No.: 0.0003 Length: 351
Score: 121.50 Matches: 58
Percent Similarity: 33.5% Conservative: 10
Best Local Similarity: 28.6% Mismatches: 58
Query Match: 10.8% Indels: 77
DB: 2 Gaps: 10

US-09-920-953-2 (1-598) x US-09-252-991A-18476 (1-351)

QY 30 CACAGAGCGCGGAGCGGATGCGGCGCAAGAGCTGTTGATGACCTGGCGGCGC 89
DB 131 HisArgAlaAlaGlyArgGlyProAlaAlaGlyProSerGlyProArgProGlyArg 150
QY 90 AGA-----AGCATGAAGCTGGCGGTGACACCTTCTACGATAAGT 131
DB 151 LysProAlaValArgProAlaAlaAlaAlaProAla----- 163
QY 132 GCTGCTGACCGCGAGCTGCTGCTTCTTCAGTCCCTGGA-----CATGCA 179
DB 164 -----ProGlyLysAspProArgArgArgArgGlyAspGlnGluProHisArg 180
QY 180 AGAGCAGAGATGAAGCAGGTCAAGTTCATGAGCTTGTGTTGGCGGAGCAGCAATA 239
DB 181 AlaAlaArgArgAlaGlyGlyAlaHis-----ArgProTrpArg---ArgProLeu 197
QY 240 CAAAGCGCGAGCATGTACGACGACACGCCCATCTGTCAAGCGCGCGCTGACCA 299
DB 198 ProGlyProAspHisProArgGlyGlyGlnProAlaGlyGlyIleProHisAla----- 215
QY 300 CGCCCACTTTCACAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGTCAA 359
DB 216 -----AlaIleArgArgGlyArgGln 222
QY 360 -----GCAGATGTATCCAGCA-----CGCGCGCGG 386
DB 223 AlaLeuArgAlaGlyArgGlnProAlaProAspArgProLeuHisArgArgArgArg 242
QY 387 AGTGTGTGAGTCCACCGCGAGATTTGACTTNCACCAACTGCGCACCACCACTGATT 446
DB 243 ProGlyAlaValAlaProAlaAlaGlyLeuGlyAsnLeuAlaGluGlyGlnAlaGln----- 260
QY 447 TTCATTAAACCAACCCAGCGCTGAGCGCTCATTCATTCATTTGAGCGCGGAGCGCCAG 506
DB 261 -----GlyArgArgAla 264
QY 507 TTGCGC-----AGCGCGCCAGCGCGCGCGCGAGC 536
DB 265 GlyProArgArgArgArgAlaAlaAlaArgHisLeuArgProProArgProArgArg 284
QY 537 CTGCAATC 545
DB 285 LeuArgVal 287

RESULT 13
US-09-252-991A-20161
; Sequence 20161, Application US/09252991A
; Patent No. 6551795

Search completed: February 27, 2006, 09:14:41
Job time : 39 secs

This Page Blank (uspto)